

**From:** Chan, Christina  
**Sent:** Wednesday, January 12, 2005 6:55 PM  
**To:** Ramirez, Delia; STIC-Biotech/ChemLib  
**Subject:** RE: rush search 09/965825

Please rush. Thanks Chris

*Chris Chan*

TC 1600 New Hire Training Coordinator and SPE 1644  
(571)-272-0841  
Remsen, 3E89

-----Original Message-----

**From:** Ramirez, Delia  
**Sent:** Wednesday, January 12, 2005 6:25 PM  
**To:** Chan, Christina  
**Subject:** rush search 09/965825

Hi Christina,

Please approve the following interference search: seq id no: 1, 4 and 2 in the nucleic acid databases.

Thank you,

Delia M. Ramirez, Ph.D.  
Patent Examiner  
Recombinant Enzymes-Art Unit 1652  
USPTO  
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70  
Alexandria, VA 22314  
(571) 272-0938  
delia.ramirez@uspto.gov

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: 1/12/05  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence: # \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

3

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Result No.	Score	Query Match	Length	DB	ID	Description
1	366.2	11.3	1746	4	US-09-543-681A-4139	Sequence 4139, App
2	362.8	11.2	1749	4	US-09-489-039A-4884	Sequence 4884, App
3	305.2	9.4	1719	4	US-10-096-571-1	Sequence 1, App11
4	269.4	8.3	1737	4	US-09-252-991A-7335	Sequence 7335, App
5	227.4	7.0	1293	4	US-09-489-039A-4905	Sequence 4905, App
6	164.2	5.1	1103	4	US-09-252-991A-7413	Sequence 7413, App
C 7	164.2	5.1	1113	4	US-09-252-991A-7281	Sequence 7281, App
C 8	155	4.8	1454	4	US-10-096-571-7	Sequence 7, App11
9	152.8	4.7	1448	4	US-10-096-571-8	Sequence 8, App11
10	138.8	4.3	7900	4	US-08-956-171E-138	Sequence 138, App1
11	138.8	4.3	7900	4	US-08-781-986A-138	Sequence 138, App1
C 12	129.6	4.0	798	4	US-09-252-991A-7166	Sequence 7166, App
13	110.2	3.4	1746	4	US-09-107-532A-3181	Sequence 3181, App
14	101.6	3.1	1761	3	US-09-134-001C-1619	Sequence 1619, App
15	100.4	3.1	2577	4	US-09-252-991A-8458	Sequence 8458, App
16	100.4	3.1	2754	4	US-09-252-991A-8530	Sequence 8530, App
17	99.6	3.1	672	4	US-09-252-991A-14411	Sequence 14411, App
C 18	99.6	3.1	1530	4	US-09-252-991A-14293	Sequence 14293, App
C 19	99.6	3.1	3594	4	US-09-252-991A-14262	Sequence 14262, App
C 20	87.2	2.7	260	3	US-08-735-545-24	Sequence 24, App1
C 21	87.2	2.7	260	3	US-09-449-083-24	Sequence 24, App1
C 22	81.2	2.5	1443	4	US-09-252-991A-8318	Sequence 8318, App
23	74.6	2.3	4411529	3	US-09-103-840A-1	Sequence 1, App1
24	73	2.2	4403765	3	US-09-103-840A-2	Sequence 2, App1
C 25	70.8	2.2	1515	4	US-09-543-681A-2618	Sequence 2618, App
C 26	68.8	2.1	2111	4	US-10-086-571-11	Sequence 11, App1
27	68.8	2.1	2111	4	US-10-096-571-13	Sequence 13, App1

C	28	65.2	2.0	1833	2	US-08-403-852D-6	Sequence 6, Appl1
C	29	65.2	2.0	1833	3	US-08-510-646B-6	Sequence 6, Appl1
C	30	65.2	2.0	1833	3	US-09-231-818-B	Sequence 6, Appl1
C	31	65.2	2.0	1833	4	US-09-637-359B-6	Sequence 6, Appl1
C	32	65.2	2.0	3390	3	US-09-550-328-1	Sequence 1, Appl1
C	33	65.2	2.0	3390	4	US-09-767-878-B	Sequence 1, Appl1
C	34	61.4	1.9	1776	4	US-09-583-110-152	Sequence 1, Appl1
C	35	60.8	1.9	2841	2	US-08-452-071-1	Sequence 1, Appl1
C	36	60.8	1.9	2841	3	US-09-231-065-1	Sequence 1, Appl1
C	37	60.8	1.9	2841	3	US-09-011-762-5	Sequence 5, Appl1
C	38	59.8	1.9	1587	4	US-09-489-039A-2568	Sequence 2568, Ap
C	39	59.8	1.8	2502	4	US-08-961-537-48	Sequence 48, Appl1
C	40	58	1.8	4403765	3	US-09-103-840A-1	Sequence 2, Appl1
C	41	58	1.8	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
C	42	57	1.8	1689	4	US-09-489-039A-840	Sequence 840, App
C	43	55.8	1.7	1830121	4	US-09-557-884-1	Sequence 1, Appl1
C	44	55.8	1.7	1830121	4	US-09-563-990A-1	Sequence 1, Appl1
C	45	55.8	1.7	1830121	4	US-10-339-960-1	Sequence 1, Appl1

## ALIGNMENTS

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RESULT 1
US-09-543-681A-4139
: Sequence 4139, Application US/09543681A
: Patent No. 6505709
: GENERAL INFORMATION:
: APPLICANT: GARY BRETON
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
: TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 2709.1002-001
: CURRENT APPLICATION NUMBER: US/09/543,681A
: CURRENT FILING DATE: 2000-04-05
: PRIOR APPLICATION NUMBER: US 60/128,706
: PRIOR FILING DATE: 1999-04-09
: NUMBER OF SEQ ID NOS: 8344
: SEQ ID NO 4139
: LENGTH: 1746
: TYPE: DNA
: ORGANISM: Proteus mirabilis
: US-09-543-681A-4139

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Query Match	11.3%;	Score 366.2;	DB 4;	Length 1746;
Best Local Similarity	-53.7%;	Pred. No. 1.7e-104;		
Matches 899;	Conservative 0;	Mismatches 758;	Indels 18;	Gaps 6;

Oy	AGGTTGAAGGAAATTTATGGTTTGGTGGGAGACAGCTTATCCGATCGTGGAAATCGT	908
Db	72 AGGTGTGAACGTATTTGGGGGGTGCAGGGCGATTCAATTGAATGGATTTAACTGAATAGCTT	131
Oy	909 CCGCAATCAAGT--ATTGAGTGGGTGCACGTTTCGAATGAGGAAAGCGGGCGCTTTGC	965
Db	132 GCGCAAAATGGGTATCCATTGATGATGGGACACGCGCATAGAAAGTCGGGCTTTTTC	191
Oy	966 AGCGGAGCGGAATCGATTGATCACTGGGGAGCTGGCAGTANGTGTGCTTCTTGTGAGTCC	1028
Db	192 CGCCGAGACGAAAGCGGCTATCAATGGTGAATTAGCGCTTTGTGCCGCTCTGTGGAC	251
Oy	1026 TGGAAACACACCTGATTCAGGGTCTTTATGATTCGATCGAAATGGTGGCAAGGT	1085
Db	252 AGTAACTTACACTTAATTATATGCACTTTTGAATTGTCAATGTATCATGTCTCCGGT	311
Oy	1086 GGCATCGCTAGCAATTTCCGATGGCCAGATGGTTCGACGTTCTCCAGAGAAACCA	1144
Db	312 AGCGATTCGCGCTATATCTCTGTGCAATTTGGTAGTAATTAATTTCAGAAATCA	371
Oy	1146 TCCGAGATTTGTTTAAGGAAATGCTGTGTACTGCGAGATGGTGAATGGTGTGACCA	1208
Db	372 TCTCCAAAGATTATTTGTGAATGTAGCACTAATTGGAAATTAGTCTTAATCCGATCA	431
Oy	1206 GGGTGAACGATTTTGATCAACGGGATTCAGTCCACCATGGCGGGTAAAGGTGTCTGGT	1265

D	b	432	GATCCCAAAATTCGGTATACGCTATACGCAACCGCTATTTTGAAAAAGGCTTCGGT	491
Q	y	1266	GTATGATTTCTCGTGTATTCGTTAAGAAAGCAGAGTGAACGTATTAATTCATTC	132
D	b	492	GGTGTATTTACCCGATATGATGACGTTAAACCGCTCCAGAAAGATGCCATTAATTC	550
Q	y	1326	CACATATTTCTTCGGCACTCCGTGGGTGCCGAAATCCCTACTGAGCTGCACGCTGGT	1385
D	b	551	--GGATACCACTAAATCAACCACTGATTAATGCCGAATCGTTTGAATGAATAATTC	608
Q	y	1386	GAAGGCCATTAACAACCTTAAGTCTGCACTTTGTTCTGCGTGCAGCGGTGAAGATTC	1445
D	b	609	TGAGGCACTGAATTAACCTTAATAATCACTTAATGTGGTGCCGTTTGCTCAACG	668
Q	y	1446	TCGCGCCAGATGTGTGAGTTGGCGGAGAAATTAAATCAACCGATGCGGCATGCCGTGG	1505
D	b	669	ACATGATGAAGTGTGAATTAAGCAACACTTAATAAGCCCTGTGTGCAAGCACTACG	728
Q	y	1506	TGCTAAGCACTACATCCAGCATAGAAATCGTTTGAAGTGCAGATGTGCGCTCTTGG	1565
D	b	729	TGGAAAGATATCTTGAAGTGAATATCAATGACGTGGAAATGAACGGCTTATACG	788
Q	y	1566	TTACGGCGCTGCGTGGATGCGTCCAATGACGCGATCTGCTGATTTATTTGGTACGA	1625
D	b	789	TTTTTATCGCGGTATCAACCAATGGAATGCCATTTAGTGTGATGATCA	848
Q	y	1626	TTTCCCTATTTCTGATTTCTCTCT--AAAGCAACGTTGCCAGGTGATATCAACG	1682
D	b	849	ATTCCTTATCGGCTTCTTATCTCCCAACCTAATATTAATCAATTAAGCTTAATCC	908
Q	y	1683	TGGGCACATTTGTCGACGTACACACGCTGAAGTATCCGCTGACCGGTATGTTCTGCAC	1742
D	b	909	AAGTATATTTGGCTCACATTCGCATGTGTATATGCTTTGTTGAGATGTCAAAGCAAC	968
Q	y	1743	AATCGAAATATTTTTCCTCATGTGAAGAAAAACAGATGTTCTCTCTGATCCGAT	1802
D	b	969	CCTTATGCAATTAACAACCGCATTAATAAGAAACATACCGCAATCTTGATGCTTC	1028
Q	y	1803	GCTCAAGGACACACGACCGTAAGTGACTCGGTGTAGACGTACACATTAACGTGCA	1862
D	b	1029	GTTAAA--ACATTTATGCTAAAGCACGMAAGATTTGATCATTTGCTCAACCTAATG-	1084
Q	y	1863	GAAGCATGTGCTATTCAACCTGATACGTGTGCTCTATTTTGAACGAGCTGCGATTA	1922
D	b	1085	--AGGTAGTTGATTCACCTCCAGTATTTAGCAAGCTGATTAATGAAATTAAGCAACGA	1142
Q	y	1923	GGATGCGGTAACTGTGAGTACCGGCATGTGCATGTGTGCGATCGAGTACATCGA	1982
D	b	1143	TGATCGGATATTTACCTGTGATGTGTGGACCCCAACAGTTTGGGACGACGTTA---CG	1199
Q	y	1983	GAATCCGAGGGAACGCGCACTTTGTGGGTCAATTCGCGACGCGACGATGCTTAATGC	2042
D	b	1200	GAATAATGATGTAAACGTCTTTAATTTGTTGCTATTTAACCAAGGCTCAATGCGAATGC	1259
Q	y	2043	GTTCCTCATTCGATTTGTCGCAAAAGTGTGATCGAAACCGCAGGTGATCCGATGTC	2102
D	b	1260	GATGCGCAACCTATTTGATTTCAAGCACTGACAGAAACGTCAAGTTGTGCGATGTG	1319
Q	y	2103	TGCGCATGTGTTGGGCATGCTGCGGGTGAAGCTTGAACCGTTAAGTGAACCACT	2162
D	b	1320	CGGTAGCGTGTGTTTACATGTTAATGGGTGATTCATCTCAATGCTCAATGAATCT	1379
Q	y	2163	TCCGCTAAGCGTGTGTGTTTAAACAACAGTTCTTTGGCATGCTGTAATGAAATGAA	2222
D	b	1380	ACCGGTAAAGTGTGATTTTATATAACAGCGTATTAAGTTTGTGGCATTGAATGAA	1439
Q	y	2223	CGTGAAGGACAGCGAATTTGTGCTGACCATGTAGGAATGAAATTTGCAAGATTCG	2282
D	b	1440	AGCGGGGCGCTATTTGACTGATGACACCGAATTAACATAATCTGATTTTGCCTATTCG	1499
Q	y	2283	GGCGGCTGCGGGTATCAAAATCGTACGATCAACCGATTCGAAAGAAATTCGAGACACT	2342
D	b	1500	CAATGCGCGGGAATTAAGGTATTCGCGTTGAGAAAGCGCAAGATCTTGATGAAGCAAT	1559

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QY      2343 AGCTGAGGCATTGGCATATCTCGAACCCTGACTACTGATGATATGTCAACGATCTTAATGC 2402
Db      1560 AAAAACGCCCTTTAAACATGATGAGCCCTGTTATTTGTGAATGTGTMAACCCAAAACAAGA 1619
QY      2403 GCTGTGATCCCAACCAACATCAGTGGGAACAGTGATGGATTTGCAAGGCGGCAC 2462
Db      1620 GCCTTCATGCGCTCCGGAAATTAATTGAGCAGGCCCAAAGGTTTTAGCTTGTATATGAT 1679
QY      2463 CCGAAGCGTCTTGTGTGAGAGATGAGAGCGATGATGATCTGGCCCCGTGAAAC 2517
Db      1680 GAAGGCATTATTAATGATGCTGTGGCGATGAAATAGTGCAATTTAGCGAAAAACAAC 1734

RESULT 2
US-09-489-039A-4884
; Sequence 4884, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 4884
; LENGTH: 1749
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-4884

Query Match          11.2%; Score 362.8; DB 4; Length 1749;
Best Local Similarity 52.8%; Pred. No. 2e-103;
Matches 909; Conservative 0; Mismatches 792; Indels 21; Gaps 5;

QY      802 ATGGCACACAGCTAGACGACAACTAATTTAGCACTTTGAAAGCTCAAGTGTGAGCGA 861
Db      31 ATGAACACGACCGTGGCGCATTAACCTTGCCAAACGCTGGAACAGGCCGCGGTGAACGT 90
QY      862 ATTATGSGTTGGTGGTGTGACAGCCTTAAT---CCGATCGTAGATGCTGTGCGGCAATCA 918
Db      91 ATCTGGGCGTCAACCGAGATTTCCCTCAATGATTTAGCCGATAGCCTTAACCGATGGGC 150
QY      919 GATATGAGTGGGTGTCACGTTCCGAATGAGAAAGCGCGCGGTTGCAAGCCGTGCGGAA 978
Db      151 ACGATCGACTGAATGCCACCCGACGAMAAGGTGCGCGCTTTGCGCGCTGCGCGGAA 210
QY      979 TCCTTGATCACTGGGGAGCTGGCAGTATNGTCTCTCTTCTGTGGTCCCTGGAACAACACAC 1038
Db      211 GCGCAGCTGACCGCGAGAGCTGGCGGCTCTGCGCGGCTCTCTGCGACCGGGCAACTGCAC 270
QY      1039 CTGATTCAGGGTCTTTATGATTCGATCGATAAGTGTGCGAAGGTGTGGCCATCGTAGC 1098
Db      271 CTGATTAACGGTTTGTGTGACTGTCTCATCGAACCATGTCCCGGGTGTGGCCATGCGCGCC 330
QY      1099 CATTTTCGAGTGGCCGAGATTGTTGTCAGCGTTCTTCAGAGAAAGCATCCGAGATTGTTG 1158
Db      331 CACATCCCATTCAGCGAAATCGCGACGCGCTATTTTGAAGAAACCAATCTCTCAGAGACTG 390
QY      1159 TTTAAGGAATGCTCTGTGTTATCTGCGAGATGATGATGATGATGATGATGATGATGATGAT 1218
Db      391 TTCGCGACAGTGCAGCCATTACTGCGAACTGTCTCCACGCGCGGAGAGACGATCCCGCAG 450
QY      1219 TTGATCAGCGCATTCAGTCCACATGCGGGGTAAAGGTGTGTGCGGTGATGATTTCTT 1278
Db      451 CTGCGACGTGCGAGTGTGAAGGAGGATGATTAACCGGGGCTCTGCGGTGTGTGTGCGCC 510
QY      1279 GGATGATGCTTAAGGAAGACGAGAGTGAACGGTATTTTCAATTTCCAATTTCTTCT 1338
Db      511 GGGAGATGTGGCGGTAAAGGCTGCTCCGTAAGAGCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 570
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QY	1339	GGCACTCCGTCGAGGTTTC	CCGGATCTCTA	CTGAGGCTGCA	GGCGTCGTCGAGGCAATTAC	1398		
Db	570	--GCTGCCAGCGGTCA	CCCGCGGAA	AGAGCTGCGCA	AGCTGCGCACTTAATTCG	627		
QY	1399	AACGTAAGTCGTCA	CTTTGTTCTG	CGCGTGGCGGCGTA	GAAGATGTCGCGCGCAGGTG	1458		
Db	628	TACTTCAGCAATATCG	CGCTCATG	TGGCGGCA	GCAGCGGTGCGCGGCCCA	CGAAGACTG	687	
QY	1459	TTGGAAGTTGGGGA	GAATTTAAT	CACCGATCGG	GCATGCGCTGCGGTGAAGCAATAC	1518		
Db	688	GTGAGTTTCGACG	CCAAATTAAAG	CCCCCATCTG	CCACGCGCTGCGCGCAAAAGACAC	747		
QY	1519	ATCCAGCATGA	GAATCCGTTTGA	GGGTGGGCAATG	CTGGCTGCTTGGTTAGGGGCGCTCG	1578		
Db	748	GTGAGTAGACAA	CAACCCGTA	CGATGTTGGGCA	TAGACCGGGCTGATTTGGGCTTCTTCTTGCG	807		
QY	1579	GTGATGCGCTCA	ATGAGCGGANTCTG	CTGATTTCTAT	TGAGGTAACGGAATTTCCCTTAATCT	1638		
Db	808	TTCCACACATAG	ATGAAGCCGAT	ATCCGTGATCTG	CTGGGCAACCAATTTCCCTATGCG	867		
QY	1639	GATTTCTTCTTAA	AAGAC--AAC	GTGCCCCAGGTG	ATATCAACGCTGCGCA	CAATTTGT	1695	
Db	868	GCCTTCTACCA	ACCGACGCGAA	AAATATTCAGAT	TCGACATCAACCCCGGACAGATCGGC	927		
QY	1696	CGAGGTACCA	CGGTGAAGAT	ATCCGTGACCGGTG	ATGTTGCTGCA	CAATGAAATATT	1755	
Db	928	GCACACATTA	AGGTGTCGAT	AGGCGCTGTGTGGCGAT	TATTAATGCA	CCCTGAAGCGCTG	987	
QY	1756	TTGCCTCATG	TGAAGAA	AAAAAGATGTTCTCTT	CTGTGATCGGATCT	CAAGGACAC	1815	
Db	988	CTGCGCGCTG	TGAGAGAA	AAAAACGATGCCA	CTTCTCTGAT-----AA	GGCGCTG	1038	
QY	1816	GAGCGTA	GTTAGCTCGGTG	GTAGAGCGTACA	CACTAA	CGTCGAGACATGTGCT	1875	
Db	1039	GAGACATATCG	CGACGCGCGAA	AAAGGCTCGAC	CGATCTGGCTAA	ACCAGGATTAAGCC	1098	
QY	1876	ATTCAACCTGA	ATACGTTCCTCTA	TTTGAACGAGCTG	CGGATTAAGAT	TCGGGTGTT	1935	
Db	1099	ATTCAACCGCA	ATATCTGGCGCAG	ACAGATCA	GTCATTTTGGCGATGA	AGAGCAATTTTC	1158	
QY	1936	ACTGTGATAC	CGGCAATGTCAGAT	GTGTGGCATGTGGAG	GTATCATCGA	GAATCCGAGGGA	1995	
Db	1159	ACCTGTGATGTG	GGACCCCGACCGTCTG	GGCGGACGCTA	TCTC--AA	ATGAATAGGT	1215	
QY	1996	ACGCGCGACTT	TGTGGGTTCA	TTCCGCGCACG	GCACGATAGCTTA	ATGCTTCATATGCG	2055	
Db	1216	AAAGCGCGCTG	CTGGGCTGTTCA	ACACGCGCTCA	ATATGTCMA	AGCATCCCGAGGCC	1275	
QY	2056	ATTGTGTGCG	CAAGTGTATCGAA	ACCGCAGGTATCG	CGATGTGTGTGGCGAT	GTGTGT	2115	
Db	1276	ATCGCGCGCA	AGGCCACTGCGCGCGAG	GGGCGAGGTATG	TGGGCTCATGTGTGGCGGCG	CGG	1335	
QY	2116	TTTGGGCA	ATGCTCTG	GGTAGCTTTGA	CCGTGACCAATTTCCGCTGA	AGGCT	2175	
Db	1336	TTTCAAGCA	ATGCTGATGGGATTTTCTG	CTGCGCTGGCGCAGAT	GAAGCTGCGCGGTGA	AAATTT	1395	
QY	2176	GTGGGTGTTA	CAACAGTTCTTTTGGG	CATGTGTAAGTTGGAGATG	CTCGTGAAGGACAG		2235	
Db	1396	GTCACTTTTA	CAACAGCGTCTGGGCTTCTG	TGGCATGTA	GAATGAAGCCGGGGGCTAT		1455	
QY	2236	CCAGATTTGT	ACTGACATGAGGA	AGTGAATTTTCGAC	AGATTTGCGCGCGCTG	CGGCT	2295	
Db	1456	CTCACCGAC	GGTACGGAGCTC	CAAGATACCAATTTTCG	CGCATCTGCTGA	AGGCTGTGGGCT	1515	
QY	2296	ATCAATTCGT	TACGATCACCGAT	TCGGAAGAA	AGTTGCGGACAGCT	TAAGCTGA	GGCAATG	2355
Db	1516	ATCAAAAGT	ATAACCGTTGAA	AAAAGCCCTCCAG	GTGATGAAGCGCTGC	CAACCGCTTC	1575	
QY	2356	GCATATCTG	GAACCTGATCTGAT	ATGATATGCTCA	CGGATCTTA	ATGATGCGCTGTGAT	CCCA	2415
Db	1576	CGACCCGAC	GGTCTGGGTCTGTGAC	GTCTGTCTGCTCG	CAAAAGAAATCTGG	CAATCCG	1635	

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OY      2416 CCAGCAGTCACTGGGAGACAGGTCAATGGATTGAGCAAGCGCCACCGAACCGCTTT 2475
DB      1636 CCGCAGATCAAGCTGTGAGAGAGCCCAAGGCTTTAGCCTGATATATGCTGCGGGCGATCATC 1655
OY      2476 GGTGAGGAGATGAGAGCGATGATTCATCTGTGGCCGCTTCCAGC 2517
DB      1696 AGCGGGCGCGCGGATGAGGTGATCGAACTGGCGAACAACCAAC 1737

RESULT 3
US-10-096-571-1
; Sequence 1, Application US/10096571
; Patent No. 6623944
; GENERAL INFORMATION:
; APPLICANT: RIEPING, MECHTHILD
; TITLE OF INVENTION: Process for the preparation of D-pantothenic acid and/or salts thereof
; FILE REFERENCE: 211499
; CURRENT APPLICATION NUMBER: US/10/096,571
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: DE 10112102.4
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/304,776
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1719
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1716)
; OTHER INFORMATION:
US-10-096-571-1

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OY      2416  CCAACCATCAGTGGGAACAGGTGATTCAGCAAGGGCCACCCGAACGCTTT 2475
DB      1616  CCGAGATCAAGCTCGAGCAGGCCCAAGGCTTTAGCCCTTAATGCTGCGGCCATCATC 1655
OY      2476  GGTGAGAGTAGAGAGCCGATGATTCATTCGCCCCGCTTGCANC 2517
DB      1696  AGCGGCGCGCGCATGAGTGCATCGAACTGGCGAAGCAAC 1737

RESULT 3
US-10-096-571-1
; Sequence 1, Application US/10096571
; Patent No. 662394
; GENERAL INFORMATION:
; APPLICATION: RIPPING. MECHTHILD
; TITLE OF INVENTION: Process for the preparation of D-pantothenic acid and/or
; FILE REFERENCE: 211499
; CURRENT APPLICATION NUMBER: US/10/096,571
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: DE 10112102.4
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/304,776
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 1
; LENGTH: 1719
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1716)
; OTHER INFORMATION:
US-10-096-571-1

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OY      2416  CCAACCATCAGTGGGAACAGGTGATTCAGCAAGGGCCACCCGAACGCTTT 2475
DB      1616  CCGAGATCAAGCTCGAGCAGGCCCAAGGCTTTAGCCCTTAATGCTGCGGCCATCATC 1655
OY      2476  GGTGAGAGTAGAGAGCCGATGATTCATTCGCCCCGCTTGCANC 2517
DB      1696  AGCGGCGCGCGCATGAGTGCATCGAACTGGCGAAGCAAC 1737

RESULT 3
US-10-096-571-1
; Sequence 1, Application US/10096571
; Patent No. 662394
; GENERAL INFORMATION:
; APPLICATION: RIPPING. MECHTHILD
; TITLE OF INVENTION: Process for the preparation of D-pantothenic acid and/or
; FILE REFERENCE: 211499
; CURRENT APPLICATION NUMBER: US/10/096,571
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: DE 10112102.4
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/304,776
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 1
; LENGTH: 1719
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1716)
; OTHER INFORMATION:
US-10-096-571-1

```

Db 481 GGGAGCGTGGCGTTAAACCTGCGCCAGAAAGGGC---AACATGACCTGATCATGCG 537  
 QY 1339 GGCACCTCTGTGGGTTTCCCGATCCATCTGAGCTGCAAGCGTGTGGAGGCGATTAAAC 1398  
 Db 538 CCACAAACAGTCTGTACGCGCGAAGAAAGAGTTACGCAAACTGCGCACCTGTGCGCT 597  
 QY 1399 AACGTTAAGTCTGTCACTTTGTTCTGCGGTGCGGCGGTGAAGAAATCTCGCGCGAGGTG 1458  
 Db 598 TATTCAGCAATATCCGCTGATGTGTGAGCGGTGCGCGGGGCGCATAAAGTTA 657  
 QY 1459 TTGGAGTTGGCGGAGAAAGTTAAATCAACGATCGGGCATGCGCTGGGTGTAAGCAGTAC 1518  
 Db 658 GTTGAATTTGCGCGGAAATTAAGCGCTATTGTTCAATGCCCTCGCGGTAAAGAAAT 717  
 QY 1519 ATTCAGCATAGAAATCCGTTGAGGTGCGCATGTCTGCGCTCTGTTAGCGCGCTGCG 1578  
 Db 718 GTCGAATACGATATCCGATGATGTGGAAATGACCGGTTAATGCGCTTCTGCGAGT 777  
 QY 1579 GTGATGCGTCCAAATGAGCGGATCTGCTGATTTCTATTGGTACGGAATTTCCCTATTCT 1638  
 Db 778 TTCCATACCATGATGAACGCCGACGTTAGTCTACTCGGACGCAATTTCCCTACCGC 837  
 QY 1639 GATTTCCTTCTTA---AAGACAAAGTTGCCAGGTGATATCAACGTTGCGCAATTTGT 1695  
 Db 838 GCCTTCTACCCGACCGATGCCAAATCAATTGATTTGATTCACCCAGCGCATCGGC 897  
 QY 1696 CGAGCTACCAAGGTGAATCCGCTGACCGGTGACCGGTGATTTGCGAAACAATCAATATTT 1755  
 Db 898 GCTCAACACAAAGTGAATATGGCACTGGTCCGCGATATCAAGTGAATCTCCGTCATTTG 957  
 QY 1756 TTGCTCATGTGAAGGAAAGAAACAGATGCTTCTTCTTGTATCGGATGCTCAAGCAAC 1815  
 Db 958 CTTTCATTGTGTGAAGAAAGCGAATGCAATTTCTGATTAAGCGCTGGAAGATTAC 1017  
 QY 1816 GAGCGTAAGTTAGCTGCTGTGTAGAGACGTACACATTAACGTGCAAGAAAGCATGTGCT 1875  
 Db 1018 CGCAGCGCCGCAAAAGGCTGAGCATTTAGCTTAACCGAGC-----AGAAAGCC 1068  
 QY 1876 ATTGACCTGAAATACCTTGTCTTATTTTGAACGAGCTGCGGATGAAGATGCGGTGTT 1935  
 Db 1069 ATTACCCGCAAAATCTGCGCAGCAAAATTAATTTTTCGCGCATGACGCTATTTTC 1128  
 QY 1936 ACTGTGATACCGGATGTCATGTGTGAGATGCGGATGATCAATCGAATTCGAGAGGA 1995  
 Db 1129 ACCTGTACCTGTGTACCGCAAGCTGTGCGCGCATGTTATCT---AAAATGAACGCG 1185  
 QY 1996 ACGGCGCACTTTGTGGTTCAATTCGCGCACGCAAGATGCTATGCGTCTCAATGCG 2055  
 Db 1186 AAGGTGCGCTGTAGGTTGTTTAAACACGTTTCATGCTAACGCCATGCGCAGGCG 1245  
 QY 2056 ATTGTGCGCAAAAGTGTGATTCGAAACCGGCAAGTATGCGCATGTGTGCGATGTGCT 2115  
 Db 1246 CTGGGTGCGAGCGGACAGACAGCAAGACGTCAAGTGTGCGCATGTGTGCGAT 1305  
 QY 2116 TTGGGCAATGCTGTGGGTAGCTTCTGACCGTTAACTGCAACAATTCCGCGTAAGGT 2175  
 Db 1306 TTTAGCATGTGTATGCGGATTTCTCTGATAGTGCATGAACTTGCAGTGAATTT 1365  
 QY 2176 GTGGTGTAAACAAGTCTTTGGGCAATGTGAAGTGTGAGATGCTGTGAGGAGACG 2235  
 Db 1366 GTGCTCTTAAACAAGCGTGTGCGCTTTGTGCGCATGAGATGAAGCTGTGTGCTAT 1425  
 QY 2236 CCAGAAATTTGTACTACCATGAGAAAGTATTCGAGAGATTTGCGCGGCTGCGGCT 2295  
 Db 1426 TTGACAGAGCGGACGCAATCAACAGCAACAATTTGCGCATTTGCGGAAGCGTGC 1485  
 QY 2296 ATCAAAATCGGTAGCATCAACGATTCGAAAGAAAGTTCGAGACAGCTAGTGAAGCATTTG 2355  
 Db 1486 ATTAACGGTATCCGTGTGAAGAAAGGTGTAAGTGAAGCCCTGCAACGCGCTTTC 1545  
 QY 2356 GCATATCTGACCTGTATCTGATCATATCTGCAAGATCTTAATGCGCTGTGATTCGA 2415  
 Db 1546 TCATATGACGCGT 1605

QY 2416 CCAACATCACTGTGGAAACAGATCATGATTCAGAAAGCGGCGCAACCGCATCTTT 2475  
 Db 1606 CCGAGATCAAACTCGAAACAGGCGCAAAAGTTTACGCTGTATATGCTGTGCGCAATCATC 1665  
 QY 2476 GTGTGAGAGTAGAGCAGATGATGATCTGTGCGCGCTTGAAC 2517  
 Db 1666 AGCGAGCGCGATGATGAATGATGCAATGCGGAAACAAAC 1707  
  
 RESULT 4  
 US-09-252-991A-7335  
 ; Sequence 7335, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 7335  
 ; LENGTH: 1737  
 ; TYPE: DNA  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-7335

Query Match 8.3%; Score 269.4; DB 4; Length 1737;  
 Best Local Similarity 50.6%; Pred. No. 5.4e-74;

Matches 823; Conservatively 0; Mismatches 776; Indels 28; Gaps 6;

QY 816 CCGAAGCAATTAATTAACATTTGAGACCTTGAGACCTCAAGTGTGAAGCAATTAATGTTGCT 875  
 Db 46 CCGCAAGATCTGTGTGAAGAACCTTGAAACCGCGGCTGCGCATTTGCTATGCGATCGT 105  
 QY 876 GGGTGAACGCTTAATCCGATCTGTGATGCTGTGCTGCGCAATCAATTAATGAGTGGTGA 935  
 Db 106 CCGCAGACCTCTCAACATGTCACGACGCGCATCATGAGCCAGATTCAGTGGTGTCA 165  
 QY 936 CGTTGAAATGAGAAAGCGGCGGCTTTGCAAGCGGTGCGGAATGTTGATCACTGGAGA 995  
 Db 166 CGTGCGCAAGAAAGGCGGCTTTCGCGCGCGCGCGAGTCTTAACAGCGGACG 225  
 QY 996 GCTGCAATATGCTGCTCTTGTGTGCTGTGAAACACACACCTGATTCAGGGTCTTTA 1055  
 Db 226 CTTGACCGGCTGCGCGGCTCTGTGCGACCGGCGAGCTGTCACTTCAACAGGCTCTA 285  
 QY 1056 TGATTCGATGAAATGTGTGGAAGGTGTCATGCTGAGCCATGCTAGCCATATTCGAGTGC 1115  
 Db 286 CGAGGCGCAAGGCAACCGCGCGCGCGATGTGTGATGCAAGCAAGTGTGATCCCGCA 345  
 QY 1116 GATTGTTTCAGCTTTCTTCAGAGAAACGATCCGAGATTTTGTTAAGATGCTGTG 1175  
 Db 346 ACTGGGATGAGATTTCCAGAGAGTGTGCACTTCAAGCGGTGTACAGCAGCTGTGCT 405  
 QY 1176 TTAATGCAAGATGTGAATGTGTGAGCAGAGGTGAACGATTTTGCATACGCGATTA 1235  
 Db 406 GTTCTGTGAGCAAGTGTGACAGCCCGGAAACAGGCGCGCGGTGTGTGCGCTGTGCGCA 465  
 QY 1236 GTCCACATGCGCGGTAAAGTGTGTGCTGTGTGATGATTTCTGTGATGTGCTAAGGA 1295  
 Db 466 GCGGCGCTCAACCGCGCGCGGTGTGCGGTGTGATTCCTGCGCGCGCATC---AGCC 521  
 QY 1296 AGACGAGGTGACGTTAATTTCAATTTCACTAATTTCTTGTGCACTCCGCTGTGT 1355  
 Db 522 AGGCGAAGGTGAAGACAGACCTGCTTCTGTGTGATTTCCGCAACCGGTGTGCGCG 581  
 QY 1356 CCGGATCTTAATGAGCTGACAGCGCTGTGAGGCGATTAAACAACGTTAATGTGTGAC 1415

Db 582 CCAAGCAGCCGAACTGAGAGACGTGCCCCCTGTC--TGCCCAACGGCAAGAAATCGG 639  
 Qy 1416 TTGTTTCGCGGTCGCGGCGGAGAAATGCTCGCGCGAGGTTGTGAGTTGGCGAGAA 1475  
 Db 640 CATTTAGCCGGCTCCGCTGCTCCAGGGGCCCCAGACTGCTGTGGCCCTCGCCAGCCG 699  
 Qy 1476 GATTAAATCAACGATCGGCGCATGCGCTGAGTGAAGCATATCCAGCATAGAAATCC 1535  
 Db 700 CCTCAAGCGCCCATTCGGGACACGTCGCGGCGCAAGAACTTCCTCGAGTACGAAACC 759  
 Qy 1536 GTTTAGAGTCGCGCATGTCGCTGCTGTTGTTAGCGCGCTGCGGTGAGTGCCTCAATGA 1595  
 Db 760 CTTCACATGCGCATGACCGGTATGCTCGGATGAGTCCGCTTCCACATGATGACCGA 819  
 Qy 1596 GGGGAGCTGCTGATTTGATTTGGGAGGAAATTCCTTATTCGATTTCTTCC---TAA 1652  
 Db 820 GTGCGACACCTCTCTGCTGCTGCGCGGACTTGCCTGGCGGAGTTCTATTCGAGAA 879  
 Qy 1653 AGACAAAGTTGCGCAGGTCGATATCAACGTCGCGCACTTGTGACGATACAGGTGAA 1712  
 Db 880 GGCAACCTGATTCAGGTCGACCGCGATGAGCATCTGCGGCGCGCCGCAACCCATCGA 939  
 Qy 1713 GTATCCGAGTACCGGTGATGTTGCTGCAACATCGAAATATTTGCTCATGTGAAGA 1772  
 Db 940 TCTCGGCTGAGTCGCGCAACGTATCCC-----CAGCTTTCGCTGTCGAAAGC 989  
 Qy 1773 AAAAACAAGATGCTTCTTCTTGAATCGAGTCTCAAGGCAACGAGGTTAAGTTAGCTC 1832  
 Db 990 CCGGAGAGAGCGACTTCTCTCGAGAAATGCTGAGACACGCGTGGCGCTGCTGCGGAC 1049  
 Qy 1833 GGTGTGAGAGCATACACATAAGTCAAGAAAGATGCGTCTTATCACTGTAATAGT 1892  
 Db 1050 GCTGGAAGAAAGAGAGCA-----GCCGGAAGGGGAGGTGATTCATCCGACGACCT 1103  
 Qy 1893 TGCTCTATTTTGAACAGCTGCGGATGAGATGCGGTGTTTACTGTGATACCGGCAT 1952  
 Db 1104 GGTGAGCTGCTGACAGCAGCAGCAGAGAGAGCGCTGTTTACCGCGAGCGCGGCTC 1163  
 Qy 1953 GTGCAATGTGTGAGATGCGAGATCATTCAGAAATCCGAGAGAAACGCGCACTTTGTGG 2012  
 Db 1164 GGCATGATGTGTGCTGTGTGCTCATCTCA---GCACCGCAAGCGCGCACCTTCAC 1220  
 Qy 2013 TTGATTCGCGCAAGGCGAAGATGCTAATGCGTCTCATGCGATGCGTGGCGAAAGTGT 2072  
 Db 1221 CAGCTGTGCTGACGCGACATGCGCAAGCCATGCCCCAGCGCTGGGGCTGAAGAGGC 1280  
 Qy 2073 TGAATGAAACCGCAGGTCGATGCGATGTGTGCGATGTGTGGCATGTGCTGGG 2132  
 Db 1281 CTACCCGAGGCGCAGGTGATCTGATCTCGGCGAGCGGCGCTGGGCATGTGCTCGG 1340  
 Qy 2133 TGAATCTGACCGTTAAGTGCACAACTTCGCTGAGGCTGTGTGTTTAAACAAG 2192  
 Db 1341 CGACTCTGACGCGCATTCAGGAAATGCTCCATCAAGGTATGTGTGTAACAATGTC 1400  
 Qy 2193 TTCTTTGGGATGATGATGATGATGATGCTGTGGAAGGACAGGCAAAATTTGTAATGA 2252  
 Db 1401 CTGCTGAACCTTCGACAGCTGGAACAGAAAGTGAAGGCGCTGTGGAACAGTACACGA 1460  
 Qy 2253 CCATGAGAAAGTGAATTTCCGAGATGTCGCGCGGCTGCGGGTATCAAAATCGTAAACAT 2312  
 Db 1461 CTGCTGAACCCGGAATTTCCGCGCTCTGCGGAAGTATGCGGTTCCACGAGAACCAAGT 1520  
 Qy 2313 CACCGATCCGAGAAAGTTGCGAGACAGTACGAGGCAATGCGATATCTGTGACTGT 2372  
 Db 1521 GACCGCTCCGAGGAGCTCGAGACGGCGGTGACAGAGTTCTCTCCAGCCCGGTCCGGC 1580  
 Qy 2373 AAGGATGATATGCTCAACGATTCCTAATGCGCTGTGATCCCAACAACATCAAGTGGGA 2442  
 Db 1581 GCTGCTGAAGTGAATCAACCTCTGCGAGAGTGTGATCCGCGAAGATGAGTTCCG 1640  
 Qy 2433 ACAGGTC 2439  
 |||||

Db 1641 CCAGGTC 1647  
 RESULT 5  
 US-09-489-039A-4905/C  
 ; Sequence 4905, Application US/09489039A  
 ; Patent No. 6610836  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary Breton et. al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 ; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 2709.2004001  
 ; CURRENT APPLICATION NUMBER: US/09/489.039A  
 ; PRIOR APPLICATION NUMBER: 2000-01-27  
 ; PRIOR FILING DATE: 1999-01-29  
 ; NUMBER OF SEQ ID NOS: 14342  
 ; SEQ ID NO 4905  
 ; LENGTH: 1293  
 ; TYPE: DNA  
 ; ORGANISM: Klebsiella pneumoniae  
 US-09-489-039A-4905  
 Query Match 7.0%; Score 227.4; DB 4; Length 1293;  
 Best Local Similarity 52.0%; Pred. No. 7.6e-61;  
 Matches 641; Conservative 0; Mismatches 571; Indels 21; Gaps 5;  
 Qy 802 ATGCAACACAGCTACGAGAAACATTAATGACATTTGGAAGTCAAGTGAACGGA 861  
 Db 1218 ATGAAACAGACCGTGGCGCATACATTGCAAAACGCTGGAACAGCCGGTGAACGT 1159  
 Qy 862 ATTATGTTGTTGGGTTGACAGCTTAAT---CCGATGTCGATGCTGTCGCAATCA 918  
 Db 1158 ATCTGGGGCTACCGGAAGTTCTCTAATGATGATGACATACCTTAACCGATGGCC 1099  
 Qy 919 GATATGAGTGGGTGACGTTTGAATGAGAAAGCGGCGGCTTTCAGCGCGTGGGAA 978  
 Db 1098 ACGATGACATGATGATCCACCGGCAAGAAAGGTGCGCTTTCGCGCTGGGCGGAA 1039  
 Qy 979 TCGTTGATCACTGGGAGCTGCGAGTATGTGCTCTTCTTGTGTCTGGAACACACAC 1038  
 Db 1038 GCGAGCTGACCGCGCAGCTGCGGCTGCGCGGCTCTGCGGACCGGCAACTTCGAC 979  
 Qy 1039 CTGATTCAGGCTCTTAATGATTCGATCGAAATGTCGAAAGTGTGGCATGCTAGC 1098  
 Db 978 CTGATTAAGGTTGTTGTTGATCTGATCGAACATGTCGCGGTGCTGGCATGCGGCC 919  
 Qy 1099 CATATTCGAGTCCGACGATTTGTTGACGCTTCTTCCAGAGAAACGATCCGAGATTTTG 1158  
 Db 918 CACATCCATCCAGCGAAATCGGAGCGGCTAATTTTCAAGAAACCATCTCAGAGACTG 859  
 Qy 1159 TTTAAGGATGCTCTGTTACTGCGAGATGTGAATGTGTGTGACAGGTTGAACGAT 1218  
 Db 858 TTCCGACAGTACGACCATTACTGCACTGTCTCCAGCGCGGACGATCCGCAAGTGTG 799  
 Qy 1219 TTGATACCGGATTCAGTCCACCATGCGCGGTGAAGTGTGCGGTGATGATTCCT 1278  
 Db 798 CTGCACTGCGAGTGCCTTAAGGACATGATTAACCGCGGCTCTCGGTGTGTGTGCTCC 739  
 Qy 1279 GGTGATATCTCTTAAGAAAGACGAGTGAACGTTATTCATTTCAATTTCTTCT 1338  
 Db 738 GGGGATGTGCGCTGAAGGCGCGCCCGGAAAGCGCAGACGACATGATGATGCGCG 679  
 Qy 1339 GGCACTCTGTGTGTCTCCGATCTTACTAGAGCTGCAAGCTGTGTGAAGCGGATTAAC 1398  
 Db 678 CTGCGGAC---GGTACCCCGCGGAAAGAACTGTGCAAGCTGGGCGAGTTATTGCG 622  
 Qy 1399 AAGCTAAGTCTGTCACTTGTCTGTGCGTGGCGGCTGAAGAAATGTCCGCGGAGGTG 1458  
 Db 621 TACTCCGCAATATCGGCTCATGTGTGCGAGCGGTGCGCGCGGCCACAGAACTG 562  
 Qy 1459 TTGAGTTGCGGAGAAATTAATCAACGATCGGCGCATGCGCTGGGTGTAAGCACTAC 1518  
 |||||



SEQ ID NO 7281  
 LENGTH: 1113  
 TYPE: DNA  
 ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-7281

Query Match 5.1%; Score 164.2; DB 4; Length 1113;  
 Best Local Similarity 50.9%; Pred. No. 5.6e-41;  
 Matches 469; Conservative 0; Mismatches 443; Indels 9; Gaps 3;

QY 816 CGCGAACAATTAATGACATTTGGAAGCTCAGAGTGTGAAGCAATTAATGTTGGT 875  
 DB 1060 CGCGAAGTCTGCTGGAACCTTGGAAGCCGCGCTCCGCAATGCTTAATGCTGCT 1001  
 QY 876 GGGTGAAGAGCTTATATCCGATGCTGAGAGTGTGCTGCGCAATCAATATTAATGAGTGA 935  
 DB 1000 CGGGAACACCTTCAACATGTCACGACGCAATCATGAGCCAGATCCAGTGGTCCA 941  
 QY 936 CGTTGGAATGAGGAAGCGCGGCTTTGCAAGCCGCTGAGGATCGTTGATCACTGGGGA 995  
 DB 940 CGTGCAGCAAGAAAGCGGCGCTTGCAGCGGCGCGAGTCTTACATCAAGGAGCG 881  
 QY 996 GCTGCAATATGCTGCTTTTGTGTCTGTAAGAACACACCTGATTCAGGCTTTA 1055  
 DB 880 CTTGACCGCTGCGCGGCTCTGCGAGCCGAGCTGACCTTCATCAACGCGCTCTA 821  
 QY 1056 TGATTGCAATGAATGCTGGAAGTGTGAGCCATGCTAGCAATATTCGAGTGCCTA 1115  
 DB 820 CGAGGCCAGCGCAACCGCGCGAGTGTCTGATGCTCCAGCCAGATCTTACCCGCA 761  
 QY 1116 GATTGTTGCAAGTCTTCTTCAGAAACGATCCGAGATTTTGTTAAGATGCTCTGG 1175  
 DB 760 ACTGGGATGAGATTTCCTCCAGAGGTGACCTTCAAGCGGCTTACGCACTGTGGT 701  
 QY 1176 TTATGCGAATGTTGAATGTTGTGAGCAGGCTGAACGCAATTTGATCAACGCGATTCA 1235  
 DB 700 GTTCTGGAAGAGGTGACAGCCCGGAACAGCGCGCTGTGTGCGCTGCGCTGCA 641  
 QY 1236 GTCCACCATGCGGGTAAAGTGTGTGAGTGTGATGTTCTGTGTATATCGTAAGGA 1295  
 DB 640 GCGCGCGCTCAACCGCGCGCGAGTGTGAGTGTGATGTTCTGCGCGCGCAATC---MCC 585  
 QY 1296 AGACGAGTGAACGCTATTATTCATTTCTGAGCACTCCCTGTGAGT 1355  
 DB 584 AGGCAAGTGAAGAGCACTGCTGCTGCTGAGCAATTCGCGAACCGGTGCTGCGCC 525  
 QY 1356 CCGGATCTTACTAGAGCTGACGCTGTGTGAGGCGATTAACAACGCTAAGTCTGAC 1415  
 DB 524 CCAAGCAAGCGAATGAGAGAGCTGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 467  
 QY 1416 TTGTTCTGCGGTGCGGCGGTGAAGATGCTGCGCGCAAGTGTGAGTGTGCGGAGAA 1475  
 DB 466 CATTAAGCGCGCTGCGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 407  
 QY 1476 GATTAAATCAACGATCGGCGATGCGCTGTGTGTGAAGCAATCAACGATGAAGATCC 1535  
 DB 406 CTTCAAGCGCGCTGCGCGCAAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 347  
 QY 1536 GTTGAAGTGTGAGTGTGCGCTGCTGTTGATGAGCGCGCTGCGGTGAAGTGTGCGCAATGA 1595  
 DB 346 CTTCAATGAGGCAATGACCGGTATGCTGCGGATGAGTCCGCGCTTCCACATGATGACGA 287  
 QY 1596 GCGGATCTGCTGATTTCTATGAGGATGAGATTTTCTTATTTCTATTTCTTCT---AA 1652  
 DB 286 GTGCGAACCCTCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 227  
 QY 1653 AGACAAAGTGTGCGAGTGAATCAACGCTGCGCAATGTTGATGAGCAAGTGA 1712  
 DB 226 GCGCAACCTTATCAAGTGTGAGCGCGATGAGCAATCACTGCGCGCGCGCGCGCGCGCGCG 167  
 QY 1713 GTATCCGATGACCGGTGAT 1733  
 DB 166 TCTGCGGTGATCGCGACGT 146

## RESULT 8

US-10-096-571-7  
 Sequence 7, Application US/10096571

Patent No. 662394

GENERAL INFORMATION:

APPLICANT: RIEBING, MECHTHILD

TITLE OF INVENTION: Process for the preparation of D-pantothenic acid and/or salts th

FILE REFERENCE: 211499

CURRENT APPLICATION NUMBER: US/10/096,571

PRIOR FILING DATE: 2002-03-14

PRIOR APPLICATION NUMBER: DE 10112102.4

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: US 60/304,776

PRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn version 3.1

SEQ ID NO 7

LENGTH: 1454

TYPE: DNA

ORGANISM: Escherichia coli

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)..(1454)

OTHER INFORMATION: Multigene DNA

NAME/KEY: misc feature

LOCATION: (1)..(56)

OTHER INFORMATION: Technical-grade DNA/Residues of polylinker sequence

NAME/KEY: misc feature

LOCATION: (57)..(577)

OTHER INFORMATION: Part of the 5' region (poxB1) of the poxB gene

NAME/KEY: misc feature

LOCATION: (578)..(646)

OTHER INFORMATION: Technical-grade DNA/Residues of polylinker sequence

NAME/KEY: misc feature

LOCATION: (647)..(1398)

OTHER INFORMATION: Part of the 3' region (poxB2) of the poxB gene

NAME/KEY: misc feature

LOCATION: (1399)..(1454)

OTHER INFORMATION: Technical-grade DNA/Residues of polylinker sequence

US-10-096-571-7

Query Match 4.8%; Score 155; DB 4; Length 1454;

Best Local Similarity 53.7%; Pred. No. 5.3e-38;

Matches 345; Conservative 0; Mismatches 235; Indels 3; Gaps 1;

QY 1874 CTATTCAACCTGATTAATGCTTCTTATTTGAACGAGCTGCGGATGAAGATCGGCTGT 1933  
 DB 768 CATTCAACCGCAATATCTGCGCGAGCAATTAATGATTTTGGCGCGAGGCAATTT 827  
 QY 1934 TTACTGTGATACCGGATGATGCAATGTGTGAGTGTGAGTATGAGATTCGAGAG 1993  
 DB 828 TCACCTGTGACGTTGTGATACCGCAACGCTGTGCGGCGACGTTATCTAATAA---TGAACG 884  
 QY 1994 GAAAGCGGCACTTTGTGAGTCAATTCGCGACGCGAGATGAGTGTGAGTGTGAGTGTGAGTGT 2053  
 DB 885 GCAAGCTGTGCTTTTGTGAGTGTGATTAACAGGTTGATGAGTGTGAGTGTGAGTGTGAGTGT 944  
 QY 2054 CGATTGTGCGCAAGATGTTGATGGAACCGCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 2113  
 DB 945 GGTGTGTGTGCGGAGGAGCAAGAGCAAGATGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1004  
 QY 2114 GTTGTGAGTGTGCTGTGTGTGAGTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 2173  
 DB 1005 GTTGTGAGTGTGATGAGTGTGAGTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1064  
 QY 2174 GTGTGTGTTAACAAGTCTTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2233  
 DB 1065 TTGTGTCTTTAACAAGGCTGT 1124  
 QY 2234 AGCCGAATTTGTGATCAACATGAGAGTGAATTTGCAAGATTTGCGGCGGCTTGC 2293

RESULT 9  
US-10-096-571-8  
; Sequence 8, Application US/10096571  
; Patent No. 6623944

Query Match	4.7%	Score 152.8	DB 4	Length 1448
Best Local Similarity	53.4%	Pred. No. 2.6e-37		
Matches 344	Conservative 0	Mismatches 297	Indels 3	Gaps 1

QY	2054	CGATTGCTGGCCAAAGTTGATTCGAAACCGCCAGGTGATCGCATGTGTGGCATGTG	2113
Db	973	CGCTGGGTGGCGAGCGGACAGAGCCAGAACGTCAAGTGGTGGCCATGTGGCGCATGGCG	10322
QY	2114	GTTTGGGCAATGCTGCTGGGTGAGCTTTCGACCGTTAACTGCACCAATTTCCGCTGAAGG	2173
Db	1033	GTTTATGCAATGTGATATGGCCGATTTCTCTCAATGATGTCAGATGAAATTCGCAAGTGA	1092
QY	2174	CTGTGATGTTTAAACAAGATTCTTTGGGCATGTGTAAGTTGAGATGCTCGTGAAGGAC	2233
Db	1093	TGTGCTCTTTTAAACAACAGCGTGCAGGCTTGTGGCGATGAGATGAAGCTGTGACT	1152
QY	2234	AGCCAGAAATTTGGTACTGATCCATGACGAGGAAGATTTTCGACAGATTCGGCGGCTGGC	2293
Db	1153	ATTGATCGAGCGGACCCGAACTTACACGACACAACTTTGCCCGCATTCGGAAGCGTGC	1212
QY	2294	GTAATCAATTCGGTATCGCATCAACCGATCCGAGAAAGTTTCGCGAGCAGCTTACGAGGCA	2353
Db	1213	GCATTTACGGGTATCCGTGTGAAAAAAGCGTCAAGTTGATGTAAGCCCTTGCAACGGCCT	1272
QY	2354	TGGCATATCTCGACCTGTACTGAATCAATATCGTACGATCCTTAATGCGCTGTGCATCC	2413
Db	1273	TCTCCATCGAGCGTCCGCTGTGTGTGATGTGTGTGTGCGCAAGAAAGATTGACATTC	1332
QY	2414	CACCAACCATCACTGTGGAAACAGTCAATGATTTAGCAAGCGGCGCACCCGAACCGCTT	2473
Db	1333	CACGCGAGATCAACTGACACAGGCCAAAGTTTCAAGCTCTGATATATGCTGCGCGCAATCA	1392
QY	2474	TTGGTGAAGGATGAGAGCAATATTCGATCTTGGCCCGCTTGCAC	2517
Db	1393	TGACGGACGCGGTGATGAAGTATATGAACTGCGCAAAACAAAC	1436

RESULT 10  
 US-08-956-171E-138  
 ; Sequence 138, Application US/08956171E  
 ; Patent No. 6593114  
 ; GENERAL INFORMATION:  
 ;  
 APPLICANT: Charles Kunsch

Patrick S. Dillon  
Craig A. Rosen  
Steven C. Barash  
Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5236  
CORRESPONDENCE ADDRESS:  
ADDRESSEE:

CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956, 171E  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,996  
FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:  
NAME: Mark J. Hyman  
REGISTRATION NUMBER: 46,789  
REFERENCE/DOCKET NUMBER: PB248P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (240) 314-1224



TELEFAX: (301) 309-8439  
 INFORMATION FOR SEQ ID NO: 138:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7900 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 138:  
 US-08-956-171E-138

Query Match 4.3%; Score 138.8; DB 4; Length 7900;  
 Best Local Similarity 45.0%; Pred. No. 2.1e-32;  
 Matches 741; Conservative 0; Mismatches 887; Indels 20; Gaps 5;

820 GAACATTAATTTGACCTTTGGAAGCTCAAGGTGGAAGCGAATTATGTTGGTGGT 879  
 1589 GAAGCATTAATTTGGAAGCTTTGGAAGCTTTGGAAGCTTTGGAAGCTTTGGAAG 1648  
 880 GACAGCCTTAATCCGATCGTGAATGCTGCGCCATCAATA-----TTGAGTGGTGC 934  
 1649 GACTCAATCGACGATAGTCAATGTTACGTAAGTGAAGATCAATTTAAATTTATC 1708  
 935 AGCTTCAATGAATGAGAGCGGCGCTTTGACCGCGTGCAGATCGTTATCACTGGGG 994  
 1709 ATGTACGTCATGAAGAAAGTACCAAGCTTACGCGCTGCTGTACACAAAATTTA 1768  
 995 AGCTGACGATATGCTGCTCTTGTGCTCTGGAACACACACCTGATTCAGGCTCTT 1054  
 1769 AATATGGTGGCATTAATGATCGGTGCGCTGTTTAACTTATTAATTAATGATAGT 1828  
 1055 ATGATTCGATCGAATGATGTCGAAGGTGTTGGCCATCGTACGCAATTCGCGTCCC 1114  
 1829 ATGATGCCAAATGATGATATGTAACGCAATTAATTAATTCGACAAACGATGTAAG 1888  
 1115 AGATTTGTTGACCTTTCTTCAAGAAACGCAATCGGAGATTTGTTAAGAAATGCT 1174  
 1889 CACTTGGAACGAAGATTCACAAAGAAACAAATTTAATAATTAATGATGATGACCG 1948  
 1175 GTTACTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1234  
 1949 TTTATTAATCAACAAATGGAAGAAAGGTGACAAATGTTGAAATGTTAAACGAATTC 2008  
 1235 AGTCACCATCGGCGGTAAAGGTGATGATGATGATGATGATGATGATGATGATGATG 1294  
 2009 GTACGCAATGATGAACAAAGATGATGATGATGATGATGATGATGATGATGATGATG 2068  
 1295 AAGAAGAGTGAAGCTTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 1354  
 2069 AAAA---AATTAAAGATCAACGAATTAACAGTATGATCAACGAACCAAGTATAT 2125  
 1355 TCCCGGATCTTACGAGGCTGACGCGTGTGAGAGGATTAACAGCTTAAGTCTGCA 1414  
 2126 CACCAAAATATTAAGATCAACAAAGGCTTAACTAATTAATTAAGTAAAGAACCTG 2185  
 1415 CTTTGTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1474  
 2186 TCAATGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2245  
 1475 AGATTAATCAACGATCGGCGATGCGCTGAGTGAACAGTACATTCAGCATGAGATC 1534  
 2246 TGGCTAAATATCTGTCAATCATTCATTCATTCATTCATTCATTCATTCATTCATTC 2305  
 1535 CGTTGAGGTGCAATGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1594  
 2306 CATATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2365  
 1595 AGGCGATCTGCTGATCTATTTGGTACGAAATTCCTTATTCGATTCCTCTTAAG 1654  
 2366 AAGCGATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2425  
 1655 ACAACGTTGCCAGGTGATTAACAAGGTGCGCATTTGTGACATGACCAAGGTGAGT 1714  
 2426 AAAATATTAAGCAATTCATTAATGACA-----CAATCTTAATAATTAATGACATGTT 2479

1715 ATCCGATGACCGGATGATGCTGCAACATTCGAATATTTTCTCATGTGAAGAA 1774  
 2480 TCAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2539  
 1775 AACAATGCTTCT 1831  
 2540 ATATTAACATGTTGCTGAAGAACCATTCCTTAACAAACGTTAGAACGTTAACGGT 2599  
 1832 CGGTGATGAGACCTTACACATTAACCTGAGAGCATGTGCTTATTCACCTTAATACG 1891  
 2600 GGGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2659  
 1892 TTGCTCTATTTTGAAGAGCTGCGGATTAAGATGATGATGATGATGATGATGATGATG 1951  
 2660 TATGATCAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2719  
 1952 TGTGCAATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2011  
 2720 CAGCAAGTTTGTGCTCAATCTGATCTT---AACTTGTGTATTAATTAACAGTTTATCA 2776  
 2012 GTTATTCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2071  
 2777 TTTCAAGTTGTTAGTACAAATGATGATGATGATGATGATGATGATGATGATGATGATG 2836  
 2072 TTGATCGAAACCGCAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 2131  
 2837 CATATTCATTAATGACAAAGCAGTCTGATGATGATGATGATGATGATGATGATGATG 2896  
 2132 GTGAGCTTCTGACCGTTAAGCTGACCAACTTCGCTGAAGGCTGTGATTTAACA 2191  
 2897 AAGACTTGTGACAGCATCAATATGATTAATCTTTAATGATTAATTAATTAATTA 2956  
 2192 GTTCTTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2251  
 2957 AACAGTTAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3016  
 2252 AACATGAGAAAGTAAATTTGCGAGATGATGATGATGATGATGATGATGATGATGATG 2311  
 3017 ATTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3076  
 2312 TCACCATTCGAGAAAGATTCGCGAGCAGTCTGAGGATTTGGCATATCTGCACTG 2371  
 3077 TTAAGATGCTAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3136  
 2372 TACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2431  
 3137 CGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3196  
 2432 AACAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2495  
 3197 AAGAGCGCTTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3254

RESULT 11  
 US-08-781-986A-138  
 ; Sequence 138, Application US/08781986A  
 ; Patent No. 6737248  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Charles Kunsch  
 ; TITLE OF INVENTION: Shapyllococcus aureus Polymucleotides and Sequences  
 ; NUMBER OF SEQUENCES: 5255  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Human Genome Sciences, Inc.  
 ; STREET: 9410 Key West Avenue  
 ; CITY: Rockville  
 ; STATE: Maryland  
 ; COUNTRY: USA  
 ; ZIP: 20850  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
 ; COMPUTER: HP Vectra 486/33  
 ; OPERATING SYSTEM: MSDOS version 6.2

```

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: P5248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8504
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 7900 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-138

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Query Match      4.3%; Score 138.8; DB 4; Length 7900;
Best Local Similarity 45.0%; Pred. No. 2.1e-32;
Matches 741; Conservative 0; Mismatches 887; Indels 20; Gaps 5;

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QY 820 GAACATTAATTAACCTTTGGAAGCTCAAGGTGTGAGAGCAATTTATGTTGGTGGT 879
DB 1589 GAAGCATTTAGTTAAACATTAACGATGAGATATAGATCACTTTATGTTTCAGGA 1648
QY 880 GACAGCTTAATCCGATCGGTGATGCTGCCCAATCAGATA-----TTGAGTGGGTGC 934
DB 1649 GACTCAATGAGCCATAGTCGATAGTTTACGTACAGTAGAGATCAATTTAAATTTATC 1708
QY 935 ACCTTGAATGAGAGAGGCGGCGTTTGACCGCGTCCGGAATCGTTATCACTGGG 994
DB 1709 AGTACGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1768
QY 995 ACCTGAGATATGCTGCTTCTTGTGCTTCTGGAACACACACCTGATTCAGGCTTT 1054
DB 1769 AATCGGTGTGCAATTAAGTATGCTGCGCTGCTGTTTAACTTATTAATGATGT 1828
QY 1055 ATGATTCGATCGAATGAGTGTGAGAGGTGGCCATCGTAGCCATATCCAGGCTTC 1114
DB 1829 ATGATGCGAATATGATATGATGACGCAATTAATATCTGACCAACAGATGACG 1888
QY 1115 AGATGCTTCAAGCTTTCCAGAAACGCAATCCGAGATTTGTTAAGAAATGCTCTG 1174
DB 1889 CACTTGAACAGAAACGATTCAGAAACAAATTTACAAATTAATGAGATGACGCG 1948
QY 1175 GTTATGAGAGATGATGATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1234
DB 1949 TTTATTAATCAACAATGAAAGAGTGAATGTTGAATGTTAAGAGAGAGAGAG 2008
QY 1235 AGTCAACATGCGCGGTAAGGTGTGCTGCTGATGATTCCTGATGATTCGTAAGG 1294
DB 2009 GTACGCAATATGAACAAAGGTGTGCTGCTGATGATTCCTGATGATTCGTAAGG 2068
QY 1295 AAGACGAGGTGAGCTTATTTCAATTCACATTTCTTCTGCACTCTGTGGTGT 1354
DB 2069 AAAA---AATTAAGATGACAGAGATTAACAGTATATCAATCAACAGAGATAT 2125
QY 1355 TCCCGATCTTACAGAGCTGCGCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1414
DB 2126 CACCAAAATTAAGATCAACAAAGAGCTTTAACTAATTAATTAAGTAAAGAGCTG 2185
QY 1415 CTGTGCTGCGGTGCGGAGAGAGATGCTGCGCGAGGTGTGAGTTGGCGAGAG 1474
DB 2186 TCATGTTAATGTGTAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2245
QY 1475 AGTTTAATCAGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 1534

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DB 2246 TGGCAAAATTCCTGATCATTTCAATTAACAGCTAAACAAATCTCCGAGATGATC 2305
QY 1535 CTTTGAAGTGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1594
DB 2306 CATATAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2365
QY 1595 AGCGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1654
DB 2366 AAGCGATTTATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 2425
QY 1655 ACAAGCTTCCAGGTGATATCAACGCTGCGACATGCTGCGACATGCTGCGACATG 1714
DB 2426 AAAATATTAAGCAATCAATGAC-----CAATCTTAATATTCGACATCGTT 2479
QY 1715 ATCCGCTGACCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1774
DB 2480 TCATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2539
QY 1775 AACAGATGCTTCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1831
DB 2540 ATATTAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2599
QY 1832 CGGTGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1891
DB 2600 GCGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2659
QY 1892 TGCCTCTATTTTGAACAGCTGCGGATTAAGATGCGGTGTTATCTGTGATACCGCA 1951
DB 2660 TAATGCAATCAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2719
QY 1952 TGTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2011
DB 2720 CAGCAACGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2071
QY 2012 GTTCAATTCGCGCACGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2071
DB 2777 TTTCAAGTGTGTTAGTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2836
QY 2072 TTGATCGAAACCGCAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2131
DB 2837 CATATCAAAATGACAAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2896
QY 2132 GTGACCTTCTGACCGTTAAGCTGCAACACCTGCTGCTGCTGCTGCTGCTGCTGCTG 2191
DB 2897 AAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2956
QY 2192 GTTCTTGGGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2251
DB 2957 AACGTTAGCATTTAATTAATGAAACAAACAGCAGCTGCTGCTGCTGCTGCTGCTG 3016
QY 2252 ACCATGAGAGAGATTTGCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2311
DB 3017 ATTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3076
QY 2312 TCACCATTCGAAAGAGTTCGCAACGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTG 2371
DB 3077 TTAAGAGTGTACGAGAGATGATGCTATAGTGAAGAGGCAATTAACAGAGATGACAA 3136
QY 2372 TACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2431
DB 3137 CGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3196
QY 2432 AACAGTCAATGAGATTCAGCAAGCGGC 2459
DB 3197 AAGAGCGCTGTATGATGATGAGGC 3224

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RESULT 12
US-09-252-991A-7166/c
; Sequence 7166, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubinfeld et al.

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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 FILE REFERENCE: 107196.136  
 CURRENT APPLICATION NUMBER: US/09/252.991A  
 CURRENT FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: US 60/074,788  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US 60/094,190  
 PRIOR FILING DATE: 1998-07-27  
 NUMBER OF SEQ ID NOS: 33142  
 SEQ ID NO 7166  
 LENGTH: 798  
 TYPE: DNA  
 ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-7166

Query Match 4.0%; Score 129.6; DB 4; Length 798;  
 Best Local Similarity 52.6%; Pred. No. 3.6e-30;  
 Matches 307; Conservative 0; Mismatches 274; Indels 3; Gaps 1;

1856 ACCTGAGAGCATGTCCTTATTCACCTGTAATAGTTGCTTATTTTGAACGAGCTGG 1915  
 644 AAGCCGCAAGGAGGAGCTGATCGACGACCTGTCAGCTGCTGACACGACG 585  
 1916 CGATTAAGATGCGGTGTTACTGTGATACCGGCATGTGCATGTGCGATCGAGT 1975  
 584 CAGCGAGAGAGCGCTGTTACCGCGACGCGCGGCGATGTCTGGCTGTTGGTC 525  
 1976 ACATCGAATCCGAGAGGAGCGCGCATTTTGGGTTCACTCCGCCAGCGCATGTG 2035  
 524 ACATCCCA---GCAGGCGAGGCGCGACCCCTCACAGCTGTGTACGCGCACATGG 468  
 2036 CTATATGCGTTCCTCATGCGATTTGTGCGCAAGTTGTGATCGAAACCGCGAGTGTG 2095  
 467 CCAAGCCATGCCCCAGGCGCTGAGGCTGAGAGGCTTACCCGAGCGCAGGTGATCT 408  
 2096 CGATGTGCGCATGTGTTGGCATGCTGCTGGTGAAGCTTCTGACCGTTAAGCTGC 2155  
 407 CGATCTCGGCGAGCGGCGCTGCGCATGCTGCTGGGACCTGCTGACCGCATCAAG 348  
 2156 ACCAATCTCGCTGAGGCTGTGTGTTTAAACAAGTTCTTTTGGCGATGTGAAGTTGG 2215  
 347 AAAAATCGCGATCAAGTGTGTGTGTAACAATGCTGCTGTAACCTGTCTCAAGCTGG 288  
 2216 AGATGCTGCGGAGGAGCAGCGCAATTTGTAATGACCAATGAGGAAGTAATTTCCAG 2275  
 287 AACGAAAGTTCAGAGGCTGCTGAGACGTAACCGACTGCTCAACCCGACTTCCGCC 228  
 2276 AGATTCGCGGCGCTGCGGATATCAATCGGTACGATACCGATCCGAAAGATTGCGG 2335  
 227 GTCTCGCGAAGTATGAGCTTCCAGCGAGCGAAGTGAACGCTCCGAGAGCTCGAGA 168  
 2336 AGCAGTAGTGAAGCATTTGGCATATCTGACCTGTATGATGATATGTCACGAGATC 2395  
 167 CGCGCGGTGACAGAGTTCTCTGCCACGCGCGGTGCGGCTGCTGAGAGTGCATCAACC 108  
 2396 CTATATGCGTGTGATTCACCAACCATCACTAGTGGGAACAGTCT 2439  
 107 CTGCGAGCTGTGATGCTCGCGCAAGATGAGTTCCGCGAGTCT 64

RESULT 13  
 US-09-107-532A-3181  
 Sequence 3181, Application US/09107532A  
 Patent No. 6583275  
 GENERAL INFORMATION:  
 APPLICANT: Lynn A Doucette-Stamm and David Bush  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
 ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
 NUMBER OF SEQUENCES: 7310  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: GENOME THERAPEUTICS CORPORATION  
 STREET: 100 Beaver Street

CITY: Waltham  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02354  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: CD-ROM ISO9660  
 COMPUTER: PC  
 OPERATING SYSTEM: <Unknown>  
 SOFTWARE: ASCII  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/107,532A  
 FILING DATE: 30-Jun-1998  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/085,598  
 FILING DATE: 14 May 1998  
 APPLICATION NUMBER: 60/051571  
 FILING DATE: July 2, 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Arinello, Pamela Deneke  
 REGISTRATION NUMBER: 40,489  
 REFERENCE/DOCKET NUMBER: GTC-012  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (781)893-5007  
 TELEFAX: (781)893-8277  
 INFORMATION FOR SEQ ID NO: 3181:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1746 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: circular  
 MOLECULAR TYPE: DNA (genomic)  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Enterococcus faecium  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (B) LOCATION 1...1746  
 SEQUENCE DESCRIPTION: SEQ ID NO: 3181:  
 US-09-107-532A-3181

Query Match 3.4%; Score 110.2; DB 4; Length 1746;  
 Best Local Similarity 44.2%; Pred. No. 7.8e-24;  
 Matches 653; Conservative 0; Mismatches 803; Indels 21; Gaps 4;

914 AATCAGATATTGAGTGTGCTGACGCTTGAATGAGAGCGGCGCTTTCAGCGGCTG 973  
 137 AACCGAAATCACTCATTCAGATTCGTATGAAAGTTCGCGCATCTGCGACGCGCTG 196  
 974 CGGATGTTGATCACTGGGAGCTGGCAGTATGTGCTGCTTGTGCTGGAACA 1033  
 197 CAGATCAAAATTAACGGGAAAGTGGCGCTGCTTTCGCTTGCAGACCTGGTCCGA 256  
 1034 CACACCTGATTCAGGCTTTTATGATTCGATCGAAATGCTGCGAAGTGTGGCCATCG 1093  
 257 CACATTTGATCATGTTTGTATGATGCAAGATGACATATGCTCTATGATGCTTCT 316  
 1094 CTAGCCATATTCGAGTCCGAGATTGTTGACGTTTCTTCAGAAACGATCCGAGAGA 1153  
 317 TAGGACAGTTGCTTCAATCATGATACTAATCTTTCCAGAACTAAATGAATATC 376  
 1154 TTTTGTTAAGGAATGCTGTGTTACTGCGAGATGTGATGTGTGTGAGCAGAGTGAAC 1213  
 377 CTATTTTCGAGATGTTAGGTATTAACATGTAAGTCAAGTCAACCAAGTCTTCGCC 436  
 1214 GCATTTTGCATCAGGATTCAGTCCACATGCGGAGTAAAGTGTGTGCGGTGATGTA 1273  
 437 ATGTAGTATGATGAGCATTTAAAGCCGCTATGATGATTAAGCGCTGTATGTACTTA 496  
 1274 TTCTGTGATATGCTTAAGAGACGAGGTGACGCTACTTATTCATTCATTAATTT 1333  
 497 TCCTGTGATCTTGTGTTTGAAGAAATGACGAACAACCTTCTTCACA---CCGCTCACA 553



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QY 1534 CCGTTGAGGTCGCGATGTCGCTGCTTGGTTCACGCGCTGCGTGAATGCGTCCAT 1593
DB 760 CTTTATAGTATGTTAGTACCTAGGTAATTTGGTACTAAATCTTATCAAAATTCAA 819
QY 1594 GAGCGGATGCTGATGATTTATTTGGTACGGAATTCCTTATTTCTGATTTCTTTAAA 1653
DB 820 GATGACACTTATTAATTAATGCTGTAACAACTATCGTATGTTAATTTTACCTTAG 879
QY 1654 GACAGCTG-----CCGAGTGAATATCAACGTCGCAATGCTGACGTCACG 1707
DB 880 AAAAATTAAGTAACTATTAATGATATGATACGAAACAAATATTTGTCACGCTTTAAA 939
QY 1708 GTGAAGTATCCGATGACCGGATGATGTTGTCACCAATGCAATATTTTGCCTCATGTG 1767
DB 940 ATTATGATAGTATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 999
QY 1768 AAGGAAAAAAGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1827
DB 1000 AAGCATGTCGCAAAACGTCATCTTAGAT-----AAGCATTAAGAACGTAAGCA 1050
QY 1828 AGCTCGGTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1887
DB 1051 GTTGGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1110
QY 1888 TAGCTGCTCTATTTTGAACGAGCTGCGGATTAAGATGAGGATGATGATGATGATGATGAT 1947
DB 1111 CGTTTATGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1170
QY 1948 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2007
DB 1171 GGTATCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1227
QY 2008 GTGGGTTCATTCGCGACGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 2067
DB 1228 ATTAATTTCTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1287
QY 2068 AGTGTGATGAAACGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2127
DB 1288 ATTTGTTATCAAAACGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1347
QY 2128 CTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2187
DB 1348 ATGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1407
QY 2188 AACATGTTCTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2247
DB 1408 AACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1467
QY 2248 ACTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2307
DB 1468 ATTTGTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1527
QY 2308 CGCATGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2367
DB 1528 GTTGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1587
QY 2368 CTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2427
DB 1588 CCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1647
QY 2428 TGGGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2459
DB 1648 AACGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1679

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; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8458
; LENGTH: 2577
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-8458

Query Match      3.1%; Score 100.4; DB 4; Length 2577;
Best Local Similarity 45.5%; Pred. No. 1.2e-20;
Matches 773; Conservative 0; Mismatches 856; Indels 69; Gaps 9;

QY 802 ATGACACACAGTACGACGAAATTAATTAATGACATTTGGAAGCTCAAGGTGTAACGA 861
DB 805 ATGTCAGACACGTTGCGCATCAATTTCTGAAAGCTTGAAGCCAGTGGGGGTGAACGC 864
QY 862 ATTTATGTTTGGTGTGAACGCTTATTCGATGCTGATGCTGT-----CGCCAA 915
DB 865 GTCTTGGCTACCGACGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 924
QY 916 TCAGATTTAGTGGTGTGACGCTTTCGAAATGAGAAAGCGCGCTTTGACGCGGTGCG 975
DB 925 GAGGCAATTCATATATCCGCGTGCACAGAGAGATGCGGCTTCATGCGCGCGCC 984
QY 976 GAATGCTTATCACTGGGAGAGCTGGCAGTATGCTGCTTCTTGTGCTGGAACAA 1035
DB 985 CAGCCAGATTCACCGGAGAGTGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1044
QY 1036 CACCTATTCAGGCTCTTATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1095
DB 1045 CACTGCTGAACGCGGCTCTACGACGCGCATGATCATGACGCGGTGCTGCGCATGCTC 1104
QY 1096 AGCCATATTCGAGTGTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1155
DB 1105 GCGCAGACGCGGCTACCGGCTTGGGAGAGCACTAACAGAGAAATGATGTCAGAGC 1164
QY 1156 TTGTTAAGGAATGCTGTGTTACTGAGATGATGATGATGATGATGATGATGATGATGATGAT 1215
DB 1165 TTGTTAAGGAATGCTGTGTTACTGAGATGATGATGATGATGATGATGATGATGATGATGAT 1224
QY 1216 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1275
DB 1225 GTGCTGACGAGGCTGCGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 1284
QY 1276 CTTGTGATATTCGTAAGAAAGCGC---AGTACGCTTATTTCAATTCATCTAT 1331
DB 1285 CCAACACATGCAACAGATGCGGCGCCGAGAGCGCACGCCACAGACGCGCACGTG 1344
QY 1332 TTCTTCTGCACTCTGTGTGTTCCCGATCTCA-----CTGAGGCTGACGCG 1380
DB 1345 ATGTCGCGGTGCGCTTGTGTCAGCGCGGACCTTACGCGCGGACGCGGACCTGAGGCGC 1404
QY 1381 CTGGTGAAGCGATTAACAACGCTTAAGTCTGTCACTTTGTTCTGCGGTGCGGCGGTGAG 1440
DB 1405 GCGCGGCGATCTCTCAATGCGCGCGCGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 1464
QY 1441 AATGCTCGCGGAGGTGTTGAGTGGCGAGAAATTAATCAACGATCGGCGATGCG 1500
DB 1465 GCGCGGACCGGAACTGAAGCGGTGCGCGAGCGCTGCGCGCGGAGTGGCGCAAGCGC 1524
QY 1501 CTGGGTGTAAGCATCACTCAAGCATGAGATCCGTTTGAAGGTGCGCATGTCTGCGCTG 1560
DB 1525 CTCTGCGCAAGGCGGCTTTCGACGACCTGCGGATCGTGAACGCGCTTCATCGGCTG 1584
QY 1561 CTGGTTACGCGCGCTGCGATGCGCTCAATGAGCGGATGCTGATTTCTATTGGGT 1620

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RESULT 15
US-09-252-991A-8458
; Sequence 8458, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

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Db 1585 CTGGACCCGCGCCAGAGCATGCTGATGAGCATTTGCAACCTTGCTGATCGTGGC 1644  
QY 1621 ACGGATTTCCCTTATTTCTGATTTCTTCTTAAGAGCAAGTTGGCCAGGTGATATCAAC 1680  
Db 1645 AGCACTTTCCCTTACAGAGAGTTCTTACCAAGGCCGCGGAGGCGGTGCAGATC 1704  
QY 1681 GGTGCG-----CACATTGCTGACGTACCAAGGTGAAATATCCGGTGAACCGGTGAT 1731  
Db 1705 GACCTGATTCGCGCAACATCGGTATCCGCTATCCGATGACCAAGGCTTGTCTGGGANT 1764  
QY 1732 GTTGTCTCAACAATCGAAAAATTTTGGCTCATGTGAGAAAAAACAATGTTCTTTC 1791  
Db 1765 GCAAGGGGAACCTCGAGAGCCCTGCTGCGCTGCTGAGCAGAAAAAGCACGCGCCT-- 1822  
QY 1792 CTTGATGGATGCTCAAGGCAACGAGCGGTAGTTGAGCTCGGTGTAGAGACGTACACA 1851  
Db 1823 -----GGCGCGCGCGGTGAGCGGGGTGACGGCCAGTCGAGAGAAACCCGCGCC 1875  
QY 1852 CATACGTGAGAGAGATGTCCTATTACCTTGAATACGTTGCTCTATTTTGAACGAG 1911  
Db 1876 CAGGCCGAAGAGCCAGCCCACTCGATCAACCCGACGCGGTATTCGTTCTTGTGAG 1935  
QY 1912 CTGGCGGATAGAGATGCGGTGTTTACTGTGATACCGGATGTCGATGTGTGATGCG 1971  
Db 1936 CAACTGCCGAGCGATGCGATTCTCTGGCGCGGACAGCGGCTGCAATACCACTGTACGCC 1995  
QY 1972 AGGTACATGAGAAATCCGAGAGGAACGCGCGACTTTGTGGTTCAATCCGCAAGCGACG 2031  
Db 1996 CCGCATTCGATCGCGCCCGCGCATGCTCGGCTGCTG--TCGGCAAGCTGGCGAAC 2052  
QY 2032 ATGGCTAATGCTTGTGCTCATATGCGATGATGATGCGCAAGTTGATCGAAACCGCAGGTG 2091  
Db 2053 ATGGCAGAGGCGGTGCTCCCTTAAGCCATTCGCCGCAAGCTGCTTATCCGACGCGCGGTG 2112  
QY 2092 ATCGGATGTGTGGGATGTGTGTGTTGGGCAATGCTGTGGGTGAGCTTGTGACCGTTAAG 2151  
Db 2113 GTGGGATGTGTGGGAGCGGCGCATGACGATGAACGCAACGCCGAATGTGTACCGTG 2172  
QY 2152 CTGCACCAACTTCCGC-----TGAAGCTGTGTGTTTAAACAACAGT 2193  
Db 2173 CAGCAGTACTGGCAGCGCTGGGAACTCGCCGACTTCAATCGTGTGTGTAACAACGCGC 2232  
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Db 2233 GATCTCAACCAAGGTGACTGGGACAGCGTGCCTGGCGGCGACCCGGAGTTCAAGCCG 2292  
QY 2251 GACCATGAGGAAGTGAATTCGAGAG-----ATTGCGCGGCTGCGGGTATCAATCG 2304  
Db 2293 GCGCAGGAAGTGAATTCCTTACGCGCGGTATGCGGACATGCTCGGCTTCAAGGCGC 2352  
QY 2305 GTACGCATCAACCGATCCGAAGAAAGTTGCGAGACAGTACGAGGATTTGGCATATCT 2364  
Db 2353 ATCGCGGTGATGCGCCGAGAGCATGACGCGGCTGGGCGAGGCTTTCGCGCGCAC 2412  
QY 2365 GAACTGTACTGATTCGATATCTGTCAGGATCTTAATGCGCTGTGATCCCAACAACATC 2424  
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QY 2425 ACGTGGGAACAGGTCAATG 2442  
Db 2473 AGTTTCAGAGGCGCAAG 2490

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Job time : 282.651 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using SW model

Run on: January 15, 2005, 07:17:41 ; Search time 169.349 Seconds  
(without alignments)  
9065.911 Million cell updates/sec

Title: US-09-965-825-1

Perfect score: 2160  
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Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	366.2	17.0	1746	US-09-543-681A-4139	Sequence 4139, Ap
2	362.8	16.8	1749	US-09-489-039A-4884	Sequence 4884, Ap
3	305.2	14.1	1719	US-10-096-571-1	Sequence 1, Appl1
4	269.4	12.5	1737	US-09-252-991A-7335	Sequence 7335, Ap
5	227.4	10.5	1293	US-09-489-039A-4905	Sequence 4905, Ap
6	164.2	7.6	1083	US-09-252-991A-7413	Sequence 7413, Ap
7	164.2	7.6	1113	US-09-252-991A-7281	Sequence 7281, Ap
8	155	7.2	1454	US-10-096-571-7	Sequence 8, Appl1
9	152.8	7.1	1448	US-10-096-571-8	Sequence 8, Appl1
10	138.8	6.4	7900	US-08-956-171B-138	Sequence 138, App
11	138.8	6.4	7900	US-08-781-986A-138	Sequence 138, App
12	129.6	6.0	798	US-09-252-991A-7166	Sequence 7166, Ap
13	110.2	5.1	1746	US-09-107-532A-3181	Sequence 3181, Ap
14	101.6	4.7	1761	US-09-134-001C-1619	Sequence 1619, Ap
15	100.4	4.6	2577	US-09-252-991A-8458	Sequence 8458, Ap
16	100.4	4.6	2754	US-09-252-991A-8530	Sequence 8530, Ap
17	87.2	4.0	260	US-08-725-545-24	Sequence 24, Appl
18	87.2	4.0	260	US-09-449-083-24	Sequence 24, Appl
19	81.2	3.8	1443	US-09-252-991A-8318	Sequence 8318, Ap
20	68.8	3.2	2111	US-10-096-571-11	Sequence 11, Appl
21	68.4	3.2	2111	US-10-096-571-13	Sequence 13, Appl
22	61.8	2.8	1776	US-09-583-110-152	Sequence 152, App
23	60.8	2.8	2841	US-08-452-075-1	Sequence 1, Appl1
24	60.8	2.8	2841	US-09-231-061-1	Sequence 1, Appl1
25	60.8	2.8	2841	US-09-011-762-5	Sequence 5, Appl1
26	59.8	2.8	25002	US-08-961-527-48	Sequence 48, Appl1
27	58	2.7	4403765	US-09-103-840A-2	Sequence 2, Appl1

C	28	58	2.7	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
	29	57	2.6	1689	4	US-09-489-039A-840	Sequence 840, App
	30	55.8	2.6	1830121	4	US-09-557-884-1	Sequence 1, Appl1
	31	55.8	2.6	1830121	4	US-09-643-990A-1	Sequence 1, Appl1
	32	55.8	2.6	1830121	4	US-10-329-960-1	Sequence 1, Appl1
	33	53.4	2.5	3390	3	US-09-550-338-1	Sequence 1, Appl1
	34	53.4	2.5	3390	4	US-09-767-878-1	Sequence 1, Appl1
	35	50.6	2.3	1701	4	US-09-583-110-1223	Sequence 1223, Ap
	36	50.6	2.3	6211	4	US-08-961-527-8	Sequence 8, Appl1
	37	49.4	2.3	1947	4	US-09-489-039A-3367	Sequence 3367, Ap
	38	49.4	2.3	2365	1	US-08-363-208-1	Sequence 1, Appl1
	39	49.4	2.3	2365	3	US-09-137-478-1	Sequence 1, Appl1
	40	48.6	2.2	1800	4	US-09-252-991A-3891	Sequence 3891, Ap
	41	48.6	2.2	1824	4	US-09-252-991A-4025	Sequence 4025, Ap
	42	48.6	2.2	1875	4	US-09-252-991A-3919	Sequence 3919, Ap
	43	48.4	2.2	1689	4	US-09-489-039A-219	Sequence 219, App
	44	48.4	2.2	1664976	4	US-08-916-421B-1	Sequence 1, Appl1
	45	48.4	2.2	1664976	4	US-09-692-570-1	Sequence 1, Appl1

#### ALIGNMENTS

```

RESULT 1
US-09-543-681A-4139
; Sequence 4139, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709, 1002-001
; CURRENT APPLICATION NUMBER: US/09/543, 681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4139
; LENGTH: 1746
; TYPE: DNA
; ORGANISM: Proteus mirabilis
; US-09-543-681A-4139

Query Match      17.0%; Score 366.2; DB 4; Length 1746;
Best Local Similarity 53.7%; Pred. No. 3.2e-108;
Matches 899; Conservative 0; Mismatches 758; Indels 18; Gaps 6;

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DB 72 AGGTGTAACGCAATTTATGTTGTTGTCGACGCTTAATCCATCGTGAATGCTGT 131
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QY 434 CCGCCATCATGAT--ATTGATGTCGTCAGCTTCGAATGAGAAAGCGCGCTTTC 450
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DB 132 GCCCAAAATGGTACCATGATGATGAGGACACCCCATGAAGAAAGTCGCGCTTTC 191
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QY 491 AGCGGTGGGATGTCGTCATGTCATGAGGAGCGTGCAGTATGTCGCTTGTGTGC 550
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DB 192 CGCGGAGGAGGAGCGCTTCATGATGATGATGATGATGATGATGATGATGATGAT 251
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QY 551 TGGAAACACACACCTGATTCAGGCTTTATGATTCGATCGAATGATGATGATGATG 610
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DB 252 AGGTAACTTACATCTTAATTAATGATCTTTTATGATGATGATGATGATGATGATG 311
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QY 611 GGCATCGTACGATTCATTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 670
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QY 671 TCCGAGATTTGTTAAGAAATGCTGCTTATGTCGATGTCGATGTCGATGTCGATGTC 730
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DB 372 TCTTCAAGATTAATTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 431
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QY 731 GGTGTAACGCAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 790
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 Db 551 --GGTATCCACTAACATACCACTAGTTATGCGGAATCGTTTGAATGAAATAATCTGTC 608  
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QY 1868 AGTGAAGCATTTGGCATATCTCGGACCTGTACTGATGATATGTCACCGATCTTAATGC 1927  
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 QY 1928 GCTGTCAATCCCAACCAACATCACTGTGGAACAGTGTATGAGATTGACAGAGCGGCGAC 1987  
 Db 1620 GCTTTCATGCTCCGGAATTTAAATTGACAGGCGAAAGTTAGCTTGATATGAT 1679  
 QY 1988 CCGAAGCGTGTGTGAGAGATGAGAGGATGATGATCTGCGCCGTTGAAC 2042  
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 RESULT 2  
 US-09-489-039A-4884  
 ; Sequence 4884, Application US/09489039A  
 ; Patent No. 6610836  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary Breton et. al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 ; FILE REFERENCE: 2709.2004001  
 ; CURRENT APPLICATION NUMBER: US/09/489,039A  
 ; PRIORITY FILING DATE: 2000-01-27  
 ; PRIOR APPLICATION NUMBER: US 60/117,747  
 ; NUMBER OF SEQ ID NOS: 14342  
 ; SEQ ID NO 4884  
 ; LENGTH: 1749  
 ; TYPE: DNA  
 ; ORGANISM: Klebsiella pneumoniae  
 US-09-489-039A-4884  
  
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 Db 151 ACCATGACGTGAGTCCACCGCGCACGAAGAGTGTGCGCTTTCGCGGTGCGGGA 210  
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 QY 684 TTTAAGAAATGCTCTGTATCTGAGATGTGAATGTGTGAGACAGAGTGAAGCAT 743  
 Db 391 TTCGCGAGTGTGAGCATTAATGCGAATGTGTGCAAGCGGAGCAATCCCGAGGTG 450  
 QY 744 TTGCAATACGCAATTAATGATCAATGTGCGGTTAAAGTGTGTGTGCTGTGATGAT 803  
 Db 451 CTGCGATGTGAGTGAAGGCAATGTAATTAACCGCGCGTCTCGGTGTGTGTCGC 510  
 QY 804 GGTGATATGCTTAAGGAAGACGAGGTGACGTTATTTTCAATTTCAATTTCTTCT 863  
 Db 511 GGGATGTGCGGCTTAAGGCGCGCCCGGAAAGCGCAAGCACTGTGATATGCGGC- 569

QY 864 GGCACTCTGTGTGTTCCCGGATCTAATGAGCTGAGCGCTGTGTGAGGCGAATTAC 923  
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 QY 924 AACCGTAAGTGTGTCACTTTTGTCTGCGGTGCGGCGGTGAAGATGCTGCGCGGAGTG 983  
 DB 628 TACTCCAGCAATATCGCGCTCATGTGCGGAGCGGTGTCGCGCGGCGCCACAGGAACTG 687  
 QY 984 TTGAGTTGGGGAAGATTAAATCAACGATCCGGGCAATGCGGTGGGTGAAGAGTAC 1043  
 DB 688 GTGAGTTGCGAGCCAAATTAAGCCCAATGTCACGCGCTGCGCGGCAAGAGCAC 747  
 QY 1044 ATCCAGCANTGAAATCCCTTTGAGGTCCGCAATGTCTGCGCTGTGTTAGCGCGCTGC 1103  
 DB 748 GTGAGATACGACAAACCGGTACGATGTGTGGCAATGACCGGCTGATTGGCTTCTTCTGCG 807  
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 QY 1164 GATTTCCTCTTAAGAC--AAGTTGCCAGGTGATATCAACGGTGGCGCAATGGT 1220  
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QY 1941 CCAACCATCAAGTGGGAAAGGTGATGAGATTGACAAAGCGGCGAACCGTCTTT 2000  
 DB 1536 CCGAGATCAAGCTGAGCAGAGCGCCAAAGCTTTAGCTGTATATGTGCGGCGCATATC 1695  
 QY 2001 GTTGAGAGATGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2042  
 DB 1696 AGCGGCGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1737

RESULT 3  
 US-10-096-571-1  
 ; Sequence 1, Application US/10096571  
 ; Patent No. 6623944  
 ; GENERAL INFORMATION:  
 ; APPLICANT: RIEBING, MECHTHILD  
 ; TITLE OR INVENTION: Process for the preparation of D-pantothenic acid and/or salts th  
 ; FILE REFERENCE: 211499  
 ; CURRENT APPLICATION NUMBER: US/10/096,571  
 ; PRIOR FILING DATE: 2002-03-14  
 ; PRIOR APPLICATION NUMBER: DE 10112102.4  
 ; PRIOR FILING DATE: 2001-03-14  
 ; PRIOR APPLICATION NUMBER: US 60/304,776  
 ; PRIOR FILING DATE: 2001-07-13  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 1719  
 ; TYPE: DNA  
 ; ORGANISM: Escherichia coli  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1716)  
 ; OTHER INFORMATION:  
 US-10-096-571-1

Query Match 14.1%; Score 305.2; DB 4; Length 1719;  
 Best Local Similarity 50.7%; Pred. No. 2.2e-88;  
 Matches 873; Conservative 0; Mismatches 828; Indels 21; Gaps 5;

QY 327 ATGCAACACAGCTACGAGAAACAATTATGACATTTGGAAGTCAAGGTGAAACGA 386  
 DB 1 ATGAAACAAACGTTTGAGGCTTATATGCAAAACCTTCATTCGAGGAGTAAACGC 60  
 QY 387 ATTATGATTTGGGTGTGACAGCTTAA---TCCGATGTGATGCTGTCCGCAATCA 443  
 DB 61 ATCTGGGAGTCAAGCGAGCTCTTGAACGCTTTATGTAAGTCTTAATGCAATGCGC 120  
 QY 444 GATATGAGTGTGCAAGTTCGAATATGAGAAAGCGCGGCTTTGCAAGCGGTGCGGAA 503  
 DB 121 ACATGAGTGTGATGTCAACCCGCAAGAAAGATGCGGCTTTGCGGTGCGCTGAA 180  
 QY 504 TCGTTATCACTGGGAGCTGCGAGATGTGTGCTTCTTGTGCTCTGAAACACAC 563  
 DB 181 GCACAACTTACGGAAGATGCGGTGTGCGCGGATGTGCGGCGCCCGGCAACTGCGAC 240  
 QY 564 CTGATTAAGGTCTTATGATTCGATCGAAATGTGTGCAAGGTGTGGCATGCTAGC 623  
 DB 241 TTATTAACAGGCTGTTCATGATGCAACGCAATCACTTCGGTACTGCGGATGCGCT 300  
 QY 624 CATATTCGAGTCCCAATTTGTTGACGTTCTTCCAGGAAACGATCCGAGATTTTG 683  
 DB 301 CATATTCCTTCAGCGAAATTTGAGGCGCTATTTCAGAGAAACCCACCAAGAGCTA 360  
 QY 684 TTTAAGGAATGCTGTGTTACTGCGAGATGTGATGATGTGTGAGCAGGAGTAAACGATT 743  
 DB 361 TTCCGCAAAATGTACTATTGCGAGCTGTTCAGCCCGGAGCAGATCCCAAGATA 420  
 QY 744 TTGATACGCGATTCAGTCCACATGAGCGGATTAAGGTGTGTGCTGTGATGATTCCT 803  
 DB 421 CTGGCGATTCGATGCGCAAGCGGTGCTTAACCGTGGCGCTTTCGTTGTGTGATGCA 480  
 QY 804 GGTGATATCCCTAAGAAAGCAGAGTGAAGCTTAATTCATATTCATATTTCTTCT 863



Db 481 GGGAGCGTGGCGTTAAACCTGCGCCAGAAAGGGC---AACATGCACTGTATCATGGC 537  
 QY 864 GGCACCTCTGTGTTGTTCCCGGATCCATGAGGCTGCAAGCCTGTGTGAGGCGATTAAC 923  
 Db 538 CCACACCACTGTGTGAGCGCCGGAAGAAAGATTACGCAAACTGGCGCAACTGTGCGCT 597  
 QY 924 AAGCGTAAAGTCTGCACTTTGTTCTGCGGTGCGGCGGTGAAGAAATGCTGCGCGCAGGTG 983  
 Db 598 TATTCAGCAATATCCCTGATGTGTGCGAGGCTGGCGGCGCGCGCATTAAGATTAA 657  
 QY 984 TTGAGTTGGCGGGAAGAAATTAATCAACGATGCGGCAATCCGTGGGTGTGAAGCATAC 1043  
 Db 658 GTTGAATTTGCGCGGAAATTAAGCGCTATTTGTTCAAGCCCTGCGCGGTAAACAAAT 717  
 QY 1044 ATCCAGCATGAGAAATCCGTTTGAAGTCCGCAATGTCGCGCTGCTTGAAGCGGCGC 1103  
 Db 718 GTGCAATACGATATCCGATATGTTGTAATGACCGGGTTAATCGCTTCTGCGAGGT 777  
 QY 1104 GTGGAAGCGTCCAAATGAGCGGATCTGTGATTTCTATTGGTAAAGGATTTCCCTTATTC 1163  
 Db 778 TTTCATACATGATGAAACCGCACGTTAGTGTACTGCGCACGCAATTTCCCTAACCGC 837  
 QY 1164 GATTTCTCTCTA---AAGACAAAGTGGCCGAGGTGATATCAACGGTGGCAATTTGCT 1220  
 Db 838 GCGTTCTACCGACCGATGCGCAAAATCATTCAGATTGATTCACCGACGACGATCGGC 897  
 QY 1221 CGACGTACCAAGTAAAGTATCGGTGACCGGTGATGTTGCTGCACAAATGAAATATTT 1280  
 Db 898 GCTCACAGCAAGTGAATATGAGCACTGGTCCGCGATTCAGATGCACTCTGCGCATTTG 957  
 QY 1281 TTGCTCATGTGAAGAAATTAACAGATGTTCTCTTCTGATCCGATGCTCAAGGCAAC 1340  
 Db 958 CTTTCATTTGTGTAAGAAATTAAGCGATGTTCTGATTAAGCGCTGGAAGATTAAC 1017  
 QY 1341 GAGCGTAAAGTGAAGTGTGATGAGAGCACTACATAGTGCAGAAAGCATGTGCT 1400  
 Db 1018 CGCGACGCGCCGAAGGCGTGGACGATTAGCTAAACCGAGC-----AGAAAGCC 1068  
 QY 1401 ATTACCCCTGAATAGTTCCTCTATTTTGAACAGACTGCGCGATTAAGATGCGGTGTT 1460  
 Db 1069 ATTACCCCGCAATATCTGGCGCAGCAAAATTAATGATTTTGGCCGCGATGCGCTATTTTC 1128  
 QY 1461 ACTGTGATACCGGATGATGATGTGTGAGATGCGAGGTAAATGAGATCCGAGGGA 1520  
 Db 1129 AACTGTGATGTTGTAACCGCAACGCTGTGGCGCGCACTTATCT---AAAAATGAACGCG 1185  
 QY 1521 ACGGCGCACTTTGGGGTTCACTCCGCAACGCAAGTGTGCTATGCTGTGCTCATGCG 1580  
 Db 1186 AAGGCTGCGCTGTGATGCTTTTAAACACGATTCATGCTAAACGCAATGCGCGACGGC 1245  
 QY 1581 ATTGTCGCAAAAGTGTGATTCGAAACCGCAAGTGTATGCGCATGTGTGCGCATGTGCT 1640  
 Db 1246 CTGGGTGCGAGGGAAGACAGAACGTAAGTGTGCTGCAATGTGCGCGCATGTGCGGT 1305  
 QY 1641 TTGGGCAATGCTGTGGGTGAGCTTCTGACCGTTAAGTGTGCAACCACTTCGCGTGAAGGCT 1700  
 Db 1306 TTTAAGCATGTTGATGGCGCATTTCTCTCAGTGTGCAATGAATCTGCACTGAATAAT 1365  
 QY 1701 GTGGGTGTTAAACAAGTTCCTTGGCGCATGTGTGAAGTGTGCAATGCTGTGAGAGGACAG 1760  
 Db 1366 GTGGCTTTTAAACAAGCGTGTGGGCTTTGTGCGCATGTGAGATGAATGATGCTGTGCTAT 1425  
 QY 1761 CGAAGTTTGTGATGCACTGAGAAAGTGAATTTGCGAGAGTGTGCGCGCGCTGCGGT 1820  
 Db 1426 TTGATGAGCGGACCGCAATCAACGACACAACTTTTCCCGCATGTGCGCAACGCTGCGGC 1485  
 QY 1821 ATCAAAATCGGTATGCAATCCGATCCGAAAGAAATTTGCGAGACAGTGTAGCTAGGCAATTTG 1880  
 Db 1486 ATTACGCGGTATCGGTGTGAAGAAAGCGTCTGAAGTTGATGAAGCCCTGGAAGCGGCTTTC 1545  
 QY 1881 GCATATCTGTGACCTGTATGATGATTCATGTCACGAGATCTTAATGCGCTGTGATTCCTCA 1940  
 Db 1546 TCCATGAGACGCTCGGTGTTGGTGTGATGTGTGCGCAAGAAAGATTTGACCTTTC 1605

QY 1941 CCAACATCACTGTGGGAACAGTTCATGAGATTCAGCAAGGCGGCAACCGGATCTTT 2000  
 Db 1606 CCGCATATCAAACTCGAAGGCGCAAGGTTTACGCTGTATATGCTGTGCGCAATCATC 1665  
 QY 2001 GTGGAAGATGAGAGCATGATGATCTGCGCCGTTGCAAC 2042  
 Db 1666 AGCGACGCGGTATGATGAATGATGCACTGCGCAAAACAAAC 1707  
  
 RESULT 4  
 US-09-252-991A-7335  
 ; Sequence 7335, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 7335  
 ; LENGTH: 1737  
 ; TYPE: DNA  
 ; ORGANISM: Pseudomonas aeruginosa  
 ; US-09-252-991A-7335  
  
 Query Match 12.5%; Score 269.4; DB 4; Length 1737;  
 Best Local Similarity 50.6%; Pred. No. 9.6e-77;  
 Matches 823; Conservative 0; Mismatches 776; Indels 28; Gaps 6;  
  
 QY 341 CGCAGAACATTAATTAATGACACTTTGGAAGCTCAAGTGTGAAGGAATTAATGTTTGT 400  
 Db 46 CGCGAGATCGTCGTGAGAAACCTTGAGAACCGCGCGCTCCGCAATGCTATGAGCATGCT 105  
 QY 401 GGTGACAGCTTAAATCCGATGTGATGTGCTGTCCGCAATGATTAATGAGTGGTGA 460  
 Db 106 CGGCAACACCTTCAACATGTACCAAGCCATCATGCGACGACAGATTCAGATGAGTGTCA 165  
 QY 461 GCTTGAATGAGAAAGGCGGCTTTGACGCGCGTGGCGGAATGCTGATCACTGGGGA 520  
 Db 166 CGTGGCCACAAAGAGCGCGCTTGTGCGCGGCGCGAGTCTTAACAGCGACG 225  
 QY 521 GCTGCAATATGTCTGCTTCTGTGTGCTGTGAAACACACACTGATTCAGGGTCTTTA 580  
 Db 226 CTTGACGCGCTGCGCGCGCTCTGTGGAACCGGGGAGCTGTGATCAACGCGCTCTA 285  
 QY 581 TGAATTCGATGAATAGTGTGGAAGGTGTGGCCATGTGTAAGCCATATTCGAGTGTCCA 640  
 Db 286 CGAGGCGCGAAGCGACCGCGCGCATGTGTGATGCGCAGACAGATCTGTACCCGCA 345  
 QY 641 GATTGTTTCAAGCTTCTTCCAGAAACGATCCGAGATTTTGTTAAGAAATGCTGTGG 700  
 Db 346 ACTGGGATGAGATTTTCCAGAGATGCACTTCAAGCGGTTCAGCAGCTGTGCTGGT 405  
 QY 701 TTACTGCAATGTGTAATGTGTGAGACAGGGTGAACGATTTTGCATCAACGCGATTCA 760  
 Db 406 GTTCTGAGACAGGTGTGACAGCCCGGAACAGCGCGCGGTGTGTGCTGTGCTGTGCA 465  
 QY 761 GTCCACCATGCGGGTAAAGTGTGTGCGGTGTAAGTATTCCTGTGATGATATGCTTAAGA 820  
 Db 466 GCGGCGCTCAACCGCGCGCGCGGTGTGTGATCTGTGCGCGCGCATC---AGCC 521  
 QY 821 AAGCAGAGTGAAGGTATTAATTCATTAATTCATTTCTGTGCACTCTGTGTGTT 880  
 Db 522 AGGCAAGGTGAAGAGACAGCTGCGCTTCTGCGTGTATTTCCCGCAACGCGGTGTGCGCC 581  
 QY 881 CCGGATCTCTAGAGGCTGCAAGCGCTGTGTGAGGCGGATTAACAGCTTAAGTGTGTAC 940



Db 582 CCAGGAGCGCGAAGCTGAGGAGCGTCCCGCTCC--TGCCCAACGCAAGAGATCG 639  
 Qy 941 TTGTTCTGCGGTCGCGGTCGGAAGATCTCGCGCGAGGTCGTTGAGTTGGCGAGAA 1000  
 Db 640 CATCTACCCCGCTCGGCTCGCAGAGGCGCCACCACTTGCTGAGGCGCTCGCCGACCG 699  
 Qy 1001 GATTAAATCACCAGATCGGCGCATGCGCTGAGTGAAGCATATCCAGCATAGAGATCC 1060  
 Db 700 CCTCAAGGCGCCCATCGCGCAACGTCGCGGCGCAAGACTTCGTGATGACGAACCC 759  
 Qy 1061 GTTGAAGTCGCGCATGTCGCTGCTGCTTTGTTACGCGCGCTGCTGATGCGTCAATGA 1120  
 Db 760 CTTCAACATGGGCAATGACCGGATCTCGGGATCGAGTCCGGCTTCCATGATGACCGA 819  
 Qy 1121 GCGCGATCTGATTTATTTGAGGATTCCTTATTTCTGATTTCTTCC---TAA 1177  
 Db 820 GTGCGACACCTCTCTGCTGCTCGGCGCACTTCGCTGGGCGCACTTATCCGCAAGAA 879  
 Qy 1178 AGACAAAGTTCGCCAGTGAATATCAAGGTCGCGCATTTGGTTCGACGTACCAAGGTGA 1237  
 Db 880 GGCACCTCTGATCCAGTTCGACCGGATGCGCATGCTGCGCGCGCCGCCACCCCATCGA 939  
 Qy 1238 GTATCCGGTGAACCGGTGATGTTGCTGCAACAATCGAAATATTTTGCCTCATGTGAAGA 1297  
 Db 940 TCTCGGCTGCTCGGCGACGTGATCC-----CAGCTTTCGCTGCTGAAGC 989  
 Qy 1298 AAAAAACAGATGTTCTCTTTCATGCGATGTCGAAGCAACAGCGCTTAAGTGAAGTC 1357  
 Db 990 CCGCGAGAGCGCAGACTTCTCTGAGAAATGCTGAGAGACCGCGAGCGCTGCTCGGAGC 1049  
 Qy 1358 GATGATAGAGACGTACACATTAACGTGAGAGAGATGTCCTTATTCACCTGAATAGT 1417  
 Db 1050 GCTGAAAAAAGAGAGCA-----GCGGCAAGGCGCAGCTGATTCATTCGCGACACT 1103  
 Qy 1418 TGCCCTTATTTTGAACGAGCTGCGCGATTAAGATGCGGTGTTTACTGTGAATACCGGAT 1477  
 Db 1104 GGTGAGCTGCTGACGACGACGCGAGGAGGAGCGCTGTTACCGCGACGCGGCTC 1163  
 Qy 1478 GTGCAATGTGCGCATGCGAGATATGAGAAATCGGAGGGAAGCGCGACTTTGTGG 1537  
 Db 1164 GCGCATGTCTGTGCTGTGCTGATCCAC---GCAACGCGACGCGCGCACCTCAC 1220  
 Qy 1538 TTCAATCCGACGCGCAGATGAGCTAATGCGTTCATGCGATTTGTTGGCGAAAGT 1597  
 Db 1221 CAGCTGTTCACGCGACATAGCCCAAGCCATGCCCCAGGCGCTGGGCTGAGAGAGC 1280  
 Qy 1598 TGATCGAAACGCGCAGTGAATCGCATGTGCGCATGAGTGTGGCATGCTGCTGG 1657  
 Db 1281 CTACCCGAGGCGCAGGTGATCTGATCTCGGCGGACGCGCGCTGGCATGTCTCG 1340  
 Qy 1658 TGAGCTTTCGACCGTTAAGCTGACCAACTTCGCTGAAGGCTGTGTGTTAACACAG 1717  
 Db 1341 CGACTGTGACGCGCATTCAGSAAAACTGCCCATCAAGGTAGTGTGTAACAATGC 1400  
 Qy 1718 TTCTTTGGGCAATGAGTGAAGTGAAGTCTGTGAGGAGGACAGCGAAATTTGTAATCGA 1777  
 Db 1401 CTGCTGAACCTTCGAGCTGAAACAGAGGTGCAAGGCGCTGCTGACACTACCGA 1460  
 Qy 1778 CCATGAGAGATGTAATTTGAGAGATTCGCGCGGCTCGGGTATCAATCGGTACGAT 1837  
 Db 1461 CTGTCTGAACCGGACTTCGCGCGCTCTGCGGAGATGATCGGCTTCACGAGCAAGAGT 1520  
 Qy 1838 CACCGATTCGAAAGAAAGTTCCGAGCAGCTAGCTAGGCAATTTGGCATTCCTGACCTGT 1897  
 Db 1521 GACCGCTTCGAGGAGCTCGAGACGCGCGGTGCAAGAGTTCTCTCGCCAGCCCGGTCCGGC 1580  
 Qy 1898 ACTGATGATATTCGACGAGATCCGAATGCGTGTGATCCCAACCAATCAAGTGGGA 1957  
 Db 1581 GCTGTGACGTGATACCAACCTTCGCGAGCTGTGATGCGCGGAAGATGAGTTCGG 1640  
 Qy 1958 ACAGTTC 1964

Db 1641 CCAGGTC 1647  
 RESULT 5  
 US-09-489-039A-4905/C  
 ; Sequence 4905, Application US/09489039A  
 ; Patent No. 6610836  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary Breton et. al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 ; FILE REFERENCE: 2709.2004001  
 ; CURRENT APPLICATION NUMBER: US/09/489, 039A  
 ; PRIORITY FILING DATE: 2000-01-27  
 ; PRIORITY APPLICATION NUMBER: US 60/117,747  
 ; PRIORITY FILING DATE: 1999-01-29  
 ; NUMBER OF SEQ ID NOS: 14342  
 ; SEQ ID NO 4905  
 ; LENGTH: 1293  
 ; TYPE: DNA  
 ; ORGANISM: Klebsiella pneumoniae  
 US-09-489-039A-4905  
 Query Match 10.5%; Score 227.4; DB 4; Length 1293;  
 Best Local Similarity 52.0%; Pred. No. 3.6e-63;  
 Matches 641; Conservative 0; Mismatches 571; Indels 21; Gaps 5;  
 Qy 327 ATGGCACACAGCTACCGAGAACATTAATGACCTTTGGAAGCTCAAGGTGTAACGA 386  
 Db 1218 ATGAAACAGACCGTGGCGGCTACATTCGCAAAAGCTTGAAACAGCCGCGTAAAGT 1159  
 Qy 387 ATTATGATGTTGATGGGTCAGGCTTAAT---CCGATGCGATGCTGTCGCGCAATCA 443  
 Db 1158 ATCTGGGCGCTACCGGAGATTCCTCATATGATTTGAGCATACCTTAACCGATGGC 1059  
 Qy 444 GATATGATGATGATGACGTTTGAATGAGAGAGCGCGGTTTGACGCGTGGCGAA 503  
 Db 1098 AACATGACATGATGATGACCGCGGACGAGAGAGTTCGCGCTTTCGCGTGGCGGAA 1039  
 Qy 504 TCGTTGATCACTGGGAGGCTGACGATATGCTCTTCTTGTGCTCTGAAACACAC 563  
 Db 1038 GCGAGCTGACCGCGAGCTGCGCGCTGCGCGCTGCGCGACCGGCAACTCTCAC 979  
 Qy 564 CTGATTCAGGCTCTTATGATTCGATGCAATGATGCAAGGTTGGCCATGCTAGC 623  
 Db 978 CTGATTAACGCTTTGTTGATGCTCATGCAACCATTCGCGGTGCGCATGCGCC 919  
 Qy 624 CATATTCGAGTGCACGATTTGATTCGACGTTCTTCCAGAAACGATCCGAGATTTTG 683  
 Db 918 CACATCCCATTCACGCAAAATGCGAGGCGCTATTTTCAGAAACCATTCCTCAGAGCTG 859  
 Qy 684 TTTAAGAAATCTCTGTTACTGCGAGATGATGATGATGATGATGATGATGATGATGAT 743  
 Db 858 TTCCGAGATGACACCATTTACTGCACTGTCTCCAGCGCGGAGCATGCCAGGTG 799  
 Qy 744 TTGATACAGGATTCAGTCCACATGCGCGGTAAAGTGTGCTGTGATGATGATGATGAT 803  
 Db 798 CTGCGAGTGGGAGTGTAAAGCATTAACGCGCGCTCTGCGGTGCTGTGCTGTGCTGCT 739  
 Qy 804 GGTATATTCGCTAAGAAAGACGAGTGAAGCTTCAATTTCAATTTCAATTTCTTCT 863  
 Db 738 GCGCATGTGGCTGAAAGCGCGCGCGGAAAGCGCGCAGACCATCTGTATCAGCGCG 679  
 Qy 864 GGCATCTCTGTGTGTTCCGGAATCTTACGAGCTGACAGCGCTGTGAGAGCGATTAAC 923  
 Db 678 CTGCGGAC---GTCACCCGCGGAAAGAGAGCTGCGCAAGCTGGCGCAGCTTAATTCG 622  
 Qy 924 AAGCTAATGCTGCACTTTGTTCTGCGGTGCGCGCGCTGAAAGATGCTGCGCGCAGGTG 983  
 Db 621 TACTCAGCAATATGCGCTCATGATGCGGAGCGGTTGCGCGCGCGCGCACAGAACTG 562  
 Qy 984 TTGAGTTGGCGAGAAATTAATCAACGATCGGCGATCGCTGCTGTGTAAGCAGTAC 1043

Db 561 GTGAGTTGCGAGCAAAATTAAGCCCCCATGCTCAGCCCTGCGCGCAAAAGACAC 502  
 QY 1044 ATCCAGCATAGATCCGTTTGAGTGTGCGATGTCTGCGCTGCTTGAAGCGCGCTGC 1103  
 Db 501 GTGAGTACAGAACCGGTATGATGTGGGATACCGGGCTGATTTGCTTCTTCTGAC 442  
 QY 1104 GTGAGTGTGCTCAATGAGGCGATCTGTGATTTCTATTTGAGTACGATTTCTTATCT 1163  
 Db 441 TTCCACACATGATGAGACCGCGATACCTGATCTCTGGGACACCAAGTTCCCTATGCG 382  
 QY 1164 GATTTCCTTCTTAAAGAC---AAGTTGCGCAGGTGATATCAAGGTGCGACATTTGCT 1220  
 Db 381 GCTTTTACCAACCGACCGCAAAATTTATCAGATGACATCAACCGCGACATCGAC 322  
 QY 1221 CGAGTACACAGGTGATGATGCGGTGACCGGTGATGTTGCTGCAACAATCGAAATATT 1280  
 Db 321 GCACACAGTAAAGTCAACATGCGCTGTGGCGATTAATCAACGCTGAAGCGCTG 262  
 QY 1281 TTGGCTCATGTGAAGGAAAAACATCTTCTTCTTGAATGCGATGCTCAAGGACAC 1340  
 Db 261 CTGCGCTGTGAGAGAAACCGATGCGCACTTCTGAT-----AAGCGCTG 211  
 QY 1341 GAGCGTAACTGAGTCTGCTGTGTAAGACGTACACATTAAGTGAAGATGTGCT 1400  
 Db 210 GAGCACTATCGGAGCGCGGAAAGGGCTCGACATCTGGCTAAACCGACGATTAAGCC 151  
 QY 1401 ATTCAACCTGATATGTTGCTCTCTTATTTTGAACGAGTGGCGGATTAAGATCGGTGTT 1460  
 Db 150 ATTCAACCGCAATATCTGGCGACGACATCAATTTTTCGATGAAGATGCTCATTTTC 91  
 QY 1461 ACTGTGATACCGGATGTCATGATGTGGATGCGATGCGATGCAATCGAATTCGGAGGA 1520  
 Db 90 ACCTGTGATGTGCGACCCCGACGCTGTGGGCGGACGCTATCTC---AAATGAATGCT 34  
 QY 1521 ACGCGGACTTTGGGTTCAATTCGCGACGCGC 1553  
 Db 33 AAACCGCGCTGCTGGGCTCGTTCAACCAACGCGC 1

RESULT 6  
 US-09-252-991A-7413  
 ; Sequence 7413, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT FILING DATE: US/09/252,991A  
 ; PRIOR APPLICATION NUMBER: 1999-02-18  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 7413  
 ; LENGTH: 1083  
 ; TYPE: DNA  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-7413

Query Match 7.6%; Score 164.2; DB 4; Length 1083;  
 Best Local Similarity 50.9%; Pred. No. 1,1e-42;

Matches 469; Conservative 0; Mismatches 443; Indels 9; Gaps 3;  
 QY 341 CGCAGAACATTAATGACACTTTGAGCTCAAGGTGTAAGCGAATTTATGTTGCT 400  
 Db 42 CGCCGAGATCGTGTGAAACCTCTGAAAGCGCGCGCTCCGCCCATTTGCTATGCAATGCT 101  
 QY 401 GGGTGAACAGCTTAATCCGATCGTGTGATGCTGCGCCCATGAGATTTAGTGGTGA 460  
 Db 102 CGCGACACCTTAACCAATGATCCGACGCTCATTCATTCGACCCAGATTCAGTGGTCCA 161

QY 461 CGTTGAAATGAGAACCGCGGCTTTTGCAGCCGCTGCGAAATGCTTGAATCACTGGGA 520  
 Db 162 CTTGCGCCACGAAAGACCGCGCTTTCGCGCGGCGCGAGTCTTACATCAGCGACG 221  
 QY 521 GCTGGCAGTATGCTCTCTTGTGATCTTGAAGAACACACACTGATTCAGGCTTTA 580  
 Db 222 CTTGACCGCTGCGCGCTCTCTGCGACCGGACAGCTTCACTTCAATCAAGCGCTCTA 281  
 QY 581 TGATTCGATGAAATGATGCGAAGGTGTTGACCATCGTACGCATATTCGAGTCCCA 640  
 Db 282 CGAGGCCACCGCAACCGCGCGATGAGTGTGATGCGACAGCAGATGTTAACCCTGA 341  
 QY 641 GATTGTTCAGCTTCTTCCAGGAAACGATCCGAGATTTTGTTAAGAAATGCTCTGG 700  
 Db 342 ACTGGGATGAGATTTCCAGAGGTGCACTTCAAGCGGCTTACGCCAGCTGCTGCT 401  
 QY 701 TTACTGAGATGATGATATGATGATGAGGATGAGGATGAGGATTTTTCATCAGCGATTA 760  
 Db 402 GTTCTGAGACAGTGTCAAGCCCGGACAGGCGCGCGGCTGTGGCTTGGCTTGCCTCA 461  
 QY 761 GTCCACATGAGCGGATTAAGGTGTGTGCTGTGATGATTCCTGTGATATGCTTAAGA 820  
 Db 462 GAGCGCTCAACCGCGCGCGGTGCGGTGTGATCTTGCAGCGGACATC---AGCC 517  
 QY 821 AGACGAGGTGACGCTACTTATTCATTTCTTCTGCACTTCTTCTGCACTCTGTGTGT 880  
 Db 518 AGGCAAGGTGAGAGACACCTGCTTCTGCTGATTTCCGCAACCGGTGCTGCGCC 577  
 QY 881 CCGGATCTTACTGAGGCTGCAAGCGCTGTGTGAGGCGATTAACAAGCTTAAGTGTAC 940  
 Db 578 CAGGACCCCGAATGACAGAGCTGCGCGCTGC---TGCGCCACGCAAGAAATG 635  
 QY 941 TTTGTTCTGCGGTGGGCGGTGAAGATGCTGCGCGAGGTGTGAGTTGGCGAGAA 1000  
 Db 636 CATCTACCGCGCTCTGCTGCGACAGGCGCCACACATCTGTGTGGCGCTTCCGCGACG 695  
 QY 1001 GATTAATACCGATCGGCGATGCGCTGAGTGTGAAGACATCAACGATGAAGATCC 1060  
 Db 696 CCTCAAGGCGCCATCTGCGACAGTGTGGGCGCAAGGATCTTCTGAGTACAGAACCC 755  
 QY 1061 GTTTAGGTCGCGATGTCTGCGCTGCTTGTGTTAGCGCGCTGCGGTGATGTCGTAATGA 1120  
 Db 756 CTTCAACATGAGGACGACCGGTATGCTCGGATGAGTCCGCTTCAATGATGACCGA 815  
 QY 1121 GCGGATCTGCTGATTTCAATGGGTGACGATTTCCCTTATTCGATTTCTCTCT---AA 1177  
 Db 816 GTGGACACCTCTCTGCTGCTGCGCGCACTTGGCGGACAGTTCTATTCGACGAA 875  
 QY 1178 AGACAGCTTGCAGGTGATATCAACGATGCGACATTTGTCAGTACACGATGA 1237  
 Db 876 GCGCACCTGATTCAGGTGACCGCGATGAGTCACTGTGGCGCGCGCAACCCATGCA 935  
 QY 1238 GTATCCGCTGACCGGTATGT 1258  
 Db 936 TCTGCGCTGTGTGCGACGT 956

RESULT 7  
 US-09-252-991A-7281/c  
 ; Sequence 7281, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT FILING DATE: US/09/252,991A  
 ; PRIOR APPLICATION NUMBER: 1999-02-18  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 7281  
 LENGTH: 1113  
 TYPE: DNA  
 ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-7281

Query Match 7.6%; Score 164.2; DB 4; Length 1113;  
 Best Local Similarity 50.9%; Pred. No. 1.2e-42;  
 Matches 469; Conservative 0; Mismatches 443; Indels 9; Gaps 3;

341 CGGAGAACATTAATTAATGACCTTGAAGCTCAAGGTGAGGAATTAATGTTGGT 400  
 1060 CGCCGAGATCGTGTGAAACCCCTGGAAGCCGCCGGGTCCGCTATGTCATGCAATCGT 1001  
 401 GGGTGAACAGCTTAATCCGATCGGATGCTGTCGGCAATCAGATATGAGTGGTGA 460  
 1000 CGGCGAACCTTCAACATGTCACCGACGATCAGGACGAGATCCAGTGGATCCA 941  
 461 CGTTGCAATGAGGAAGCCGGCGTTTGACCGGATCGGAAATCGTTGATCACTGAGGA 520  
 940 CGTGGCCAGGAAGAGCGGGCGCTTCCGCGGGGGCCGAGTCTTACATCAGCGGACG 881  
 521 GCTGGCAGTATGCTGCTCTTCTTGTCTCTGAAACACACCTGATTAAGGCTTTA 580  
 880 CCTGACCGCTGCGCCGCTCTGCGGACCGGCGACCTGCACTTCAACCGCGCTTA 821  
 581 TGAATCGCATGAAATGATGCGAAGTGTGGCCATGCTAGCCATTTCCGAGTGGCA 640  
 820 CGAGGCCAGCGCAACCGCGCGCGATGCTGATGTCAGCGCAAGTCTTACCCGCA 761  
 641 GATTTGTCACGTTCTTCCAGGAACGATCCGAGATTTTGTAAAGAAATGCTTGG 700  
 760 ACTGGGATGAGATTTCCAGAGAGTGCATTCGAAGCGGTCTAGCCAGCTGCTGCT 701  
 701 TTAATCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 760  
 700 GTTCTGAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 641  
 761 GTCCACATGCGGGGTAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 820  
 640 GGGGGGCTCAACCGCGCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 585  
 821 AGACGAGGTGAGCGTACTTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 880  
 584 AGGCGACGATGAG 525  
 881 CCGGATCTACTGAGGCTGACGCGCTGTGTGAGGCGATTAACAGCTAAGTCTGTAC 940  
 524 CAGCGACGCGGAATGCAAGAGCTGCGCGCTGC--TGCCCAAGGCAAGATCGG 467  
 941 TTGTGTCGCGGTGCGGCGGTGAAGATGCTCGCGCAGGTGTGTGAGTGTGCGAGAA 1000  
 466 CATTCAGCGCGGCTCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 407  
 1001 GATTAAATCAACGATCGGAGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1060  
 406 CTCAGAGCG 347  
 1061 GTTTAGGTGCGAGTGTGCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1120  
 346 CTTCACATGAGGATGACCGGTATGCTCGGATGAGATCGGCTTCCACATGATGACCGA 287  
 1121 GGGGATGCTGCTATTTATTTGATGAGATTTCCCTTATTTGATTTCTTCT--AA 1177  
 286 GTGCGACACCTCTGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 227  
 1178 AGACAACTGTGCG 1237  
 226 GGGCAGCTTATTCAGATGACCGCGATGACGATGACGATGACGATGACGATGACGATGAC 167  
 1238 GTATCGGATGACCGGTATG 1258  
 166 TCTGGGCTGTGCGCGCGCT 146

# RESULT 8 US-10-096-571-7

Sequence 7, Application US/10096571  
 Patent No. 6623944  
 GENERAL INFORMATION:  
 APPLICANT: RIEPINC, MECHTHILD  
 TITLE OF INVENTION: Process for the preparation of D-pantothenic acid and/or salts the  
 FILE REFERENCE: 211499  
 CURRENT APPLICATION NUMBER: US/10/096,571  
 CURRENT FILING DATE: 2002-03-14  
 PRIOR APPLICATION NUMBER: DE 10112102.4  
 PRIOR FILING DATE: 2001-03-14  
 PRIOR APPLICATION NUMBER: US 60/304,776  
 PRIOR FILING DATE: 2001-07-13  
 NUMBER OF SEQ ID NOS: 14  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 7  
 LENGTH: 1454  
 TYPE: DNA  
 ORGANISM: Escherichia coli  
 FEATURES:  
 NAME/KEY: misc feature  
 LOCATION: (1)..(1454)  
 OTHER INFORMATION: Mutagenic DNA  
 NAME/KEY: misc feature  
 LOCATION: (1)..(56)  
 OTHER INFORMATION: Technical-grade DNA/Residues of polylinker sequence  
 NAME/KEY: misc feature  
 LOCATION: (57)..(577)  
 OTHER INFORMATION: Part of the 5' region (posb1) of the posb gene  
 NAME/KEY: misc feature  
 LOCATION: (578)..(646)  
 OTHER INFORMATION: Technical-grade DNA/Residues of polylinker sequence  
 NAME/KEY: misc feature  
 LOCATION: (647)..(1398)  
 OTHER INFORMATION: Part of the 3' region (posb2) of the posb gene  
 NAME/KEY: misc feature  
 LOCATION: (1399)..(1454)  
 OTHER INFORMATION: Technical-grade DNA/Residues of polylinker sequence  
 US-10-096-571-7

Query Match 7.2%; Score 155; DB 4; Length 1454;  
 Best Local Similarity 53.7%; Pred. No. 1.4e-39;  
 Matches 345; Conservative 0; Mismatches 295; Indels 3; Gaps 1;

1399 CTATTCACCTGAAATCGTTCCTCTTATTTTGAACGAGCTGGCGAATGAGATGCGGTG 1458  
 768 CATTCACCGCGAATATCTGGCGACAGCAATTAATGATTTTGGCGGATGACGCTATTT 827  
 1459 TTAATGATACCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1518  
 828 TCACCTGTGACGTTGTGACGCGCAACGCTGTGGCGCGCAAGTATCTTAAAA--TGAACG 884  
 1519 GAACGGCGCACTTTGGGTGATTCGCGACGCGAGATGCGTAAATGCGTTCATG 1578  
 885 GCAAGGTGCGCTTTAGGTGCTTTAACCAAGTTGATGAGTAAAGCCATCCGAGG 944  
 1579 CGATTGATGCGCAAGTGTGATGCAAAACCGCAGATGATGCGATGATGATGATGATGATGAT 1638  
 945 CGCTGGGTGCGGAGGAG 1004  
 1639 GTTTGGCATGCTGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1698  
 1005 GTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1064  
 1699 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1758  
 1065 TTGTGCTTTTAAACAGCGCTGTGGCTTTGTGCGATGAGATGAGATGAGATGAGATGAGAT 1124  
 1759 AGCCAGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1818





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SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781, 986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,445
REFERENCE/DOCKET NUMBER: PB248PP
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8524
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 7900 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-138

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Query Match 6.4%; Score 138.8; DB 4; Length 7900;
Best Local Similarity 45.0%; Pred. No. 7.8e-34;
Matches 741; Conservative 0; Mismatches 887; Indels 20; Gaps 5;

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QY 345 GAACATTAAATGACCTTTGGAAGCTCAAGGTGTGAAGCAATTATGTTGGTGGT 404
DB 1589 GAGCATTAGTTAAAGATTACAGCATGGGATATGATCATTGATGTTCCAGGA 1648
QY 405 GACAGCCTTAATCCGATCGTGAGTGTGCTCCGCAATCGAATA-----TTGAGTGGTGC 459
DB 1649 GACTCAATCAAGCATAGTGTGATGTTACGTACGTGAGATCAATTTAAATTTATC 1708
QY 460 ACCTTGAAATGAGGAGCGCGGCTTTGACCGCGTCCGGAATCGTTGATCACTGGGG 519
DB 1709 ATGTAGTGTGAGGAGGATGAGGATGAGCTAGCGCTGTGTTACCAAAATTAATCTGTA 1768
QY 520 AGCTGCAATGTGTGCTTCTTGTGCTGTGAAACACACACTGATTCAGGCTCTT 579
DB 1769 AATCGTGTGTGATTAATGATCGTGTGCTGCTGTTTAACTTTTAAATGTGTATGT 1828
QY 580 ATGATTCGATCGAATGTGTGCAAGGTGTGCGCATCGTACGATATTCGAGTCCC 639
DB 1829 ATGATGCAAAATGATATGATCGCAATTAATATATCGCAACAAAGATGTAACG 1888
QY 640 AGATTGTTGACGTTCTTCAGAAAGCATCCGAGATTTGTTAGAAATGCTCTG 699
DB 1889 CACTTGAAACGAAAGCATTCAGAAACAAATTTTAAATTAATGAAAGATGTAGCG 1948
QY 700 GTTACTGCAATGTGTGATGTGTGAGCAGGTGAACGATTTTGCATCCGCGATTC 759
DB 1949 TTTATATACCAATGAAATGAAAGATGACATGTGTGAAATCGTTAACAGAGCAATTC 2008
QY 760 AGTCACCATCGCGGTAAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 819
DB 2009 GTACGGCATGAGCAAAAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2068
QY 820 AAGACGAGGTGACGTATTATTCATTCATTTCTTGTGCACTCGTGTGTGTGTGTGT 879
DB 2069 AAAA--AAATTAAGATACAAAGATTAACAGTATATCAATCAAGCAACAGATGAT 2125
QY 880 TCCCGATCTCACTGAGGCTGTGAGCGCTGTGTGAGCGCATTAACAACGTTAGTCTCA 939
DB 2126 CACCAAAATTAAGATCAAAAGCGGTAAATTAATTAATTAAGTAAAGAAAGCTGT 2185
QY 940 CTTTGTTCGCGGTGCGCGGTGAAGATGTGTGCGCGAGGTGTGTGAGTGTGCGGAGA 999
DB 2186 TCAATGTTAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2245
QY 1000 AGATTAAATCAAGATCGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1059

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DB 2246 TGGCTAAATTCCTGTCAATTCATTCATCCAGCTAAACAAATCTGCGGATGATC 2305
QY 1060 CGTTGAGGTGCGGATGTCTGCGCTGTGTTAGCGCGCTGCGGATGCTCCAAATG 1119
DB 2306 CATATAGTATCGTATCTGTAGTAAATCGGTACCAAAATCTTATCAAAATGCAAG 2365
QY 1120 AGCGGATCTCTGATTCATTTGAGTACGATTTCCCTTATTCGATTTCTTCTCAAG 1179
DB 2366 AAGCGATTTTAAATTAATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2425
QY 1180 ACAAGTTGCCAGGTGATATCAACGCGTGCACATGTGTGACGATCCAGGTGAAGT 1239
DB 2426 AAAATATTAAGCATTCATTAATGACA-----CAATCTTAAATTAATGCAATCTGT 2479
QY 1240 ATCCGATGACCGGTGATGTCTGCAACATCGAAATATTTGCTCATGTGAAGAA 1299
DB 2480 TCAATTAATTAATGAGAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2539
QY 1300 AAACGATCGTCTCTTCTTGTATCGGATGCT---CAAGCACAGAGGTATGAGCT 1356
DB 2540 ATATTAAGATGTGTGTGAAAGACCATTTCTTAAACAAACGTTAGAACGTAAACGCTTT 2599
QY 1357 CGGTGTGAGAGATGATCAACATTAACGTGAGACATGTGCTATTCACCTGATATAC 1416
DB 2600 GGGATTAATGATGAGAAACAGATTAATAATTAATTAATTAATTAATTAATTAATTAAT 2659
QY 1417 TTGCTCTTATTTGAAACGAGCTGCGGATTAAGATGCGGTGTTTACTGTGATACCGCA 1476
DB 2660 TAATGATCATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2719
QY 1477 TGTGCAATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2776
DB 2720 CAGCAACGTTGTGCAATCTGATACCT---AACTGTGTGATTAATTAATTAATTAAT 2836
QY 1537 GTTATTCGCAACGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2896
DB 2777 TTTCAAGTTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2956
QY 1597 TTGATCGAAACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1656
DB 2837 CATATTCAAATGACAAAGCATGCAATCTGCTGTGAGGTGATTCAAATGATGATGATGAT 1716
QY 1657 GTGAGCTTGTGACGTTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1776
DB 2897 AAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1836
QY 1717 GTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1896
DB 2957 AACGTTAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3016
QY 1777 ACCATGAGAAAGATTTTCCAGATTTCCGCGGCTGCGGATTCAAATCGGTACGCA 1836
DB 3017 ATTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3076
QY 1837 TCACCATTCGAAAGATTTCCGAGAGCTAGCTGAGGATTTGCGCATTCAGATGATGATGAT 3136
DB 3077 TTAAGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3196
QY 1897 TACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1956
DB 3137 CGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3196
QY 1957 AACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3196
DB 3197 AAGAGCGCTGTGTATGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3224

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RESULT 12
US-09-252-991A-7166/c
; Sequence 7166, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

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QY 859 CTCTGCGACTCTCTGCTGCTCCCGGATCTCTAGGCTGAGGCTGCTGAGAGCGCA 918  
 DB 554 CTCACAAAACAAGTGATATTAACGAGAAAAGTTTGTAGCTCTTGCTTATC 613  
 QY 919 TTAAACAGCTAGTCTGTCACTTTGTTCTGCGTCCGCGCTGAAAGAAATGCTCGCGCG 978  
 DB 614 TTGAAAAAGAAAAAACAAGTCTTTATGTTGTGTCAGAGAAACGCAAAACGATTTCCGC 673  
 QY 979 AGGTGTGAGTTGGCGAGAAAGATTAAATCAACGATCGGGATGCGCTGGGTGTAGC 1038  
 DB 674 AAATCAAAAGATCTGAGAAATTTTTCAGTTCTGTGTGCTGCTGCTTCTAGAAAAAG 733  
 QY 1039 AGTACATCCAGCATGGAATCCGTTGAGTCCGCAATGTCGCTGCTGCTGCTAGCGCG 1098  
 DB 734 GAATTAATCTGTATGATTAAGAAAACCTTCTTGTTTCTGAGAGTGTCTACTTAAC 793  
 QY 1099 CTTGCGTGAATGTCATGAGAGGCGATCTGTATTTATTTGGGTACGATTTCCCTT 1158  
 DB 794 CCGGAAATAGATTTGGCAAAAGCCGATCTGATCTTATTTGTGCTGAGCGACTTCCCAT 853  
 QY 1159 -----ATTCTGATTTCTTCTTAAAGCAACGTTGCCAGGTGATATCAACGCTGCGC 1212  
 DB 854 TTGACGTCATTTTATTAATCAACGCTGATTTATCCAAATGATTCATGCTCA 913  
 QY 1213 AATTTGTCAGTACAGTACAGGTAAGTATCCGTTGACCGGTGATGTTGCTCAACATCG 1272  
 DB 914 AATTTGACGACGCAATGAACATCTTTGTCATCTCGGTGATG-----CAACA 964  
 QY 1273 AAAATATTTTCTCATGTGAAGAAAAACAGATGTTCTCTCTGATGATGATCTCA 1332  
 DB 965 CAGCTTGCAAAAGCTTTGCAAGTTAGGGGATGCTCGCCCTGCTGATGCTGTAAGCTAG 1024  
 QY 1333 AGGCAACAGAGGTAAAGTTGAGTCTGCTGAGTGAAGACGTACACATACGTCGAGAGC 1392  
 DB 1025 CAATCAAGAAATTAAGAAAAATGGGTAAATGTTGAATCTTTGAAGATGAAGAG 1084  
 QY 1393 ATGTCCTATTCACTGATATGCTGCTATTTTGAACGAGCTGCGGTAAAGATG 1452  
 DB 1085 AAGAACGATTTGTCGACAGGCTCTATTAAGAAATCAATCGATTTGCTGAAGACATG 1144  
 QY 1453 CGGTGTTTACTGTGATACCGGCAATGTCATGTCGTCATGTCGAGTACATCGAATC 1512  
 DB 1145 CGATTTTCTGACAGATGTCGGTAAACAGACTATC---CATTTCTATTCGTTTATGAATA 1201  
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 QY 1573 CTATGCGATTTGTCGCAAAAGTGTGATGAAACGCGCAGGTGATCGGATGTCGCG 1632  
 DB 1262 CAGAGGAATTTGCGCACTAAGCTAACCAAGAAAACAGATTTTACTTAAGTGTG 1321  
 QY 1633 ATGCTGTTTGGGCAATGCTGCTGCTGAGTCTTCTGACCTTAACTGCAACATTCGCGC 1692  
 DB 1322 ATGCGGGTTTGTATGTCATCAAGATATCATTTACACAAATCAATACAGCTTCCAA 1381  
 QY 1693 TGAAGCTGTGTGTTTAAACAAGTTCTTTGGGCAATGTAAGTGTGAGATGCTGTG 1752  
 DB 1382 TTATTAATGTTGCTTTGCAATGATTTCTTTGTTTCAACGAGCAACAAAGATA 1441  
 QY 1753 AGGCAACGCAATTTGTTGTAAGTACATGAGAAATGTAATTTGCAAGATTTGCGCGCG 1812  
 DB 1442 CGGAACAAAAGAAATTTGTTTATTTAGAAATGACAGATTTGCGTAAAGTTGAGAAAG 1501  
 QY 1813 CTGCGGCTATCAAAATGCTGACGATCAACGATCCGAAAGAAATTTGCGAGAGCTAGCTG 1872  
 DB 1502 CGCTGGGGCAATTAAGCTTTAAGTACAGAAATCTGCGCACTTGCATTTGCTTGTATG 1561  
 QY 1873 AGGCAATTTGCAATCTGACCTGTACTGATGATAT 1909  
 DB 1562 CAGCTGCAAAATCAAGATGCTCTGTATGATGATGAT 1598

RESULT 14  
 US-09-134-001C-1619  
 ; Sequence 1619, Application US/09134001C  
 ; Patent No. 6380370  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lynn Doucette-Stamm et al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
 ; FILE REFERENCE: GTC-007  
 ; CURRENT APPLICATION NUMBER: US/09/134,001C  
 ; PRIOR FILING DATE: 1998-08-13  
 ; PRIOR APPLICATION NUMBER: US 60/064,964  
 ; PRIOR FILING DATE: 1997-11-08  
 ; PRIOR APPLICATION NUMBER: US 60/055,779  
 ; NUMBER OF SEQ ID NOS: 5674  
 ; SEQ ID NO 1619  
 ; LENGTH: 1761  
 ; TYPE: DNA  
 ; ORGANISM: Staphylococcus epidermidis  
 US-09-134-001C-1619

Query Match 4.7%; Score 101.6; DB 3; Length 1761;

Best Local Similarity 43.6%; Pred. No. 3.6e-22;

Matches 721; Conservative 0; Mismatches 904; Indels 27; Gaps 5;

QY 345 GAACATTTAATGACACTTTGAAAGCTCAAGGTGTAAGCGAATTTATGTTGTGGGT 404  
 DB 43 GAAGCATTTGTTAAGCATTAACAACTGGAATATGATCAATTTATATGATTTCTGGC 102  
 QY 405 GACAGCCTTAATCCAGTGGTGAATGCTGCG-----CAATCAGATTTAGTGGGTG 458  
 DB 103 GACTAGATGATGCTGTGTGTATGCTTACGTCAGTCAAGATCAATTTAAATTTCTAT 162  
 QY 459 CAGTTTGAATGAGAAACCGCGCTTTGACGCGGTGCGAATCGTATGATCACTGG 518  
 DB 163 CAGTACGTCAGTAACAGTAGAGGATTTAGTGTGTAATTTACAAAATGACAGG 222  
 QY 519 GAGCTGCAATGTCGCTCTTCTGTGTCTCTGGAACACACACTGATTCAGGCTTT 578  
 DB 223 AAATTTGTTGATGCTTAAAGTATGAGTACGAGACCTGTGTATGACCTTAATTAATGATG 282  
 QY 579 TATGATTCGATCGAATGTCGCAAGGTGTTGCAATCGCTACCAATTTCCGAGTGC 638  
 DB 283 TACATGCTAAATATGATATGTAACCTCACTTATTTGTGTAACAAATATATACA 342  
 QY 639 CAGATTTGTTGAGCTTTTTCAGGAAACGATCCGAGATTTGTTAAGATGCTCT 698  
 DB 343 TTATTTAGGTACAAAATTTCTTCCAAACAGCAAAATTTCTAAATGTTGATGTTGCT 402  
 QY 699 GGTACTGCGAGATGTAATGTCGTCGAGGAGGTAACGCAATTTGATTCACGCAAT 758  
 DB 403 GTATATACCAACCAATTTCAAAAAGGATGATGATATTTGAAATTAACAAATGAGCAAT 462  
 QY 759 CAGTTCACATGCGGGTAAAGTGTGTCGCTGATGTAATCTGCTGATATGCTTAAG 818  
 DB 463 CGTACGCAATACGAGAAAAGGTCCTGTTATCATTTGTTCAAATGATCTTATAC 522  
 QY 819 GAAGACGAGTACGCTACTTATTCGAATTTCACTATTTCTTTGCGACTCTGTGCTG 878  
 DB 523 CAATAAATTTAAGCACTACAAAT---CGTCAAGTTGATACCACTAAACCAAAACAGCT 579  
 QY 879 TTCCCGATCTTACTGAGCTGTCAGGCTGTCGAGGTCGTCGAGGCTTAACAGCTAAGTGTGTC 938  
 DB 580 TCACCAAAATTTCAAAAGTATTAATAAAGAGCTAATTTATGATTAAGCTAATAAACA 639  
 QY 939 ACTTTGTTTCGCTGCGGCGGTGAAGATGCTGCGCGCAGGTGTTGAGTTGCGGAG 998  
 DB 640 GTATGCTTATTTGTTTAAAGTACAAACAGCTTAAAGATGATTAAGTAAATTTATGA 699  
 QY 999 AATATTAATCAACGATCGGGCATGCGCTGGGTGTAACAGATATCAAGATGAT 1058  
 DB 700 GCTGCAAAATTTCACTTATTTACACATTAATCTGCAAAAACAAATCTTACCTGACATCAT 759



QY 1059 CCGTTGAGTGGCATGCTGCGCTGGTGAACGGCGCTGCGTGAAT 1118  
 DB 760 CTTATAGTATGTTAGTAACTTAAAGTAAATTTGTAACAATCTTATCAACAATCA 819  
 QY 1119 GAGCGGATCTGCTGATTTCTATTGGTACGGAATTCCTTATCTGATTTCTCTTAA 1178  
 DB 820 GATGCACTTATTAATTAATGCTGTGTAACGAACTATCGTATGTTAATTAATTAATTA 879  
 QY 1179 GACAAAGT-----CCAGTGGATATCAAGTTCGCAATGTTGCGACGTAACG 1232  
 DB 880 AAAAACAATTAAAGCTATTAATGATATCAAGAAAGAAATATTTGGTGAACGCTTTAA 939  
 QY 1233 GTGAAGTATCCGCTGACCGGATGTTGCTGCAACAATGCAAAATATTTGCTCATGTG 1292  
 DB 940 ATTATGTAAGTATTTAGTGAATGTAAGTGTCTTCCATCACTACGAAAAATTT 999  
 QY 1293 AAGGAAAAAACAATGCTTCTCTTGTGATGCTCAAGGCAACGAGCGTAAGTTG 1352  
 DB 1000 AAGCATGTCAAAAAGTCCATCTTAGAT-----AAGCATTAAGAACTTAAGCA 1050  
 QY 1353 AGCTCGGTGTAAGAGTACACATTAAGTCAAGAAAGATGCTTATTCACCTGAA 1412  
 DB 1051 GTTTGGATTAATGATGAACAAGATTTGAATTAATGACAAATTCACCAATTAAGTCA 1110  
 QY 1413 TAGCTGCTCTATTTTGAACGAGCTGCGGATTAAGATGCGGTGTTACTGTGATACC 1472  
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 QY 1713 AACAGTCTTTGGGATGTAAGTGTGAGATGCTGTGAGGGAACCAAAATTTGTT 1772  
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 QY 1773 ACTGACATGAGAAAGTATTTGCGAGATTTGCGCGGCTGCGGCTATCAATCGGTA 1832  
 DB 1468 ATTGATTTTCTGATTAATGATCATGCTAAATTTGCTAAGCTGTGTGTAAGGCTAT 1527  
 QY 1833 CGCATCAACGATCGAAGAAAGTTCGCGACGCTAGCTAGGCAATTTGCAATCTGTA 1892  
 DB 1528 GTTGTGAATGATGTAAGTGTGCTTGAACAATGTTGAAGAGGAATGGCTCAAGATTT 1887  
 QY 1893 CCGTACTGATGATATGTCACGATCTTAATGCGCTGTGATCCCAACAACATCAAG 1952  
 DB 1588 CCAACAATCTTGAAGCTTCAATGTTGATCTTAATGCTGCAACATTAACAGGTAAATTTGA 1647  
 QY 1953 TGGGAACAGTCAATGGGATTCAGCAAGCGGC 1984  
 DB 1648 AACGAAAGAGCATTTGTTAAGTAATGAGGC 1679

RESULT 15  
 US-09-252-991A-8458  
 ; Sequence 8458, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 8458  
 ; LENGTH: 2577  
 ; TYPE: DNA  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-8458

Query Match 4.6%; Score 100.4; DB 4; Length 2577;  
 Best Local Similarity 45.5%; Pred. No. 1.1e-21;  
 Matches 773; Conservative 0; Mismatches 856; Indels 69; Gaps 9;  
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 DB 805 ATGTCCAGCAGCGTTGCCGATCAATTTGCTGAACGCTTGAGCCAGTGGGGGTGAAGCC 864  
 QY 387 ATTATGTTTGTGGTGAACGCTTAATCCATCTGTGATGCTGT-----CCGCAAA 440  
 DB 865 GTCTGGCTAACCAAGCGATGGATCAAGGATATATGGCCGATGGCCGCGCGCC 924  
 QY 441 TCGATATTAATGATGGTGCACGCTTCAAAATGAGAAACGCGCGTTCAGCGGTGCG 500  
 DB 925 GAGGCAATTCACATTAATCCCGCGCCACAGAGAGATGCGCGCTTCATGCGCGCGCC 984  
 QY 501 GAATCGTATCACTGGGAGCTGGCAGTATGCTGCTTGTGTGCTGGAACAACA 560  
 DB 985 CAGGCCAATTCACCGAGAGTGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1044  
 QY 561 CACCTGATTCAGGCTCTTATTAATTCGATCGAAATGCTGCAAGTGTGCTGCTGCTGCT 620  
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 QY 621 AGCCATATTCGAGTGCAGATTTGTTGCAAGCTTTCCAGAAACGATCCGAGATT 680  
 DB 1105 GGCAGAGAGCGCTACCGGTTGGGAGCGACATACAGAGAGAGTGTGCTGCAAGC 1164  
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 QY 801 CCGTGTGATTCGTAAGAAAGCGC---AGTGAAGCTACTTAATTCATTAATTCATTAAT 856  
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 DB 1405 GCGCGCGCATCTCTCAATCGCGCGCGCGGTGCGCATCTCGCGGTGCGCGCGCGCTG 1464  
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Qy 1257 GTTGTGCAACAATCGGAAATATTTTGCCTCATGTGAGGAAAAAAGATCGTTCTTC 1316  
Db 1765 GCAGGGGAAACCTTGAGGCCCTGTGCGCCGCTGCTGAGCAAGAAAAAGCACGCGCCT-- 1822  
Qy 1317 CTTGATCGATGCTCAAGGACACAGACGCTAAGTTGAGCTCGGTGTAGAGACGTACACA 1376  
Db 1823 -----GGCGCGCGCGGTGTGAGCGGCGGTGACGCGCATGTCGAGGAGCCCGCGCG 1875  
Qy 1377 CATTAAGTTCGAGAAAGCATGTGCTTATTCACCTTGAAATACGTTGCTTATTTTGAACGAG 1436  
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Qy 1437 CTGGCGGATTAAGATGCGGTGTTTACTGTGAGTACCGGATGTGCAATGTGTGATGCG 1496  
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Qy 1719 TCTTTGGCATGTGAAGTTGAGATGC---TCGNGAGGAGACGCAAAATTGTGACT 1775  
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Db 2353 ATCCGCGTGAATCCCGGAGAGCATGACGCGCGCTGGGCGGAGGCTTCCGCGCGGAC 2412  
Qy 1890 GGAAGCTGATGATGATATGTCACGATCTTAATGCGGTGATCCCAACCAATC 1949  
Db 2413 CGCCCGGTGTGTGAGGTGTGTCAACGACCCGAAAGTGTGCGGCTGTGCGCGCACATC 2472  
Qy 1950 ACGTGGAGACAGGTGATG 1967  
Db 2473 AGTTGAGAGGCGCAAG 2490

Search completed: January 15, 2005, 08:26:57  
Job time : 195.349 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using BW model

Run on: January 15, 2005, 08:14:27 ; Search time 1105.56 Seconds  
(without alignments)  
11226.071 Million cell updates/sec

Title: US-09-965-825-1

Perfect score: 2160

Sequence: 1 ttagagcgcagatctctgtgag9.....ggtcccatgagatgcctt 2160

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCR\_NEM\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEM\_PUB.seq:\*
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- 18: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US11\_NEM\_PUB.seq:\*
- 20: /cgn2\_6/ptodata/2/pubpna/US60\_NEM\_PUB.seq:\*
- 21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2160	100.0	2160	9 US-09-965-825-1	Sequence 1, Appl1
2	2160	100.0	2160	15 US-10-143-856-3	Sequence 3, Appl1
3	2160	100.0	2160	15 US-10-078-167-4	Sequence 3, Appl1
4	2160	100.0	2160	15 US-10-336-049-4	Sequence 4, Appl1
5	2160	100.0	2160	15 US-10-091-342-4	Sequence 4, Appl1
6	2160	100.0	2160	16 US-10-686-736-4	Sequence 4, Appl1
7	2160	100.0	3248	9 US-09-965-825-4	Sequence 4, Appl1
8	2160	100.0	3309400	9 US-09-738-626-1	Sequence 1, Appl1
9	1860	86.1	1860	17 US-10-781-014-85	Sequence 85, Appl1
10	1737	80.4	1737	9 US-09-738-626-2873	Sequence 89, Appl1
11	944	43.7	944	17 US-10-781-014-89	Sequence 89, Appl1
12	875	40.5	875	9 US-09-965-825-3	Sequence 3, Appl1

13	875	40.5	875	15 US-10-143-856-5	Sequence 5, Appl1
14	875	40.5	875	15 US-10-078-167-6	Sequence 6, Appl1
15	875	40.5	875	15 US-10-336-049-6	Sequence 6, Appl1
16	875	40.5	875	15 US-10-091-342-6	Sequence 6, Appl1
17	875	40.5	875	16 US-10-686-736-6	Sequence 6, Appl1
18	813.8	37.7	1734	16 US-10-282-122A-17635	Sequence 17635, A
19	551	25.5	552	17 US-10-781-014-87	Sequence 87, Appl1
20	523	24.2	9025608	15 US-10-156-761-1	Sequence 1, Appl1
21	522.6	24.2	1740	15 US-10-156-761-2067	Sequence 2067, Ap
22	397.6	18.4	1710	15 US-10-369-493-39295	Sequence 39295, A
23	397.6	18.4	1710	15 US-10-369-493-39670	Sequence 39670, A
24	397.6	18.4	1710	15 US-10-369-493-40028	Sequence 40028, A
25	381	17.6	1737	16 US-10-282-122A-12285	Sequence 12285, A
26	380.4	17.6	1716	16 US-10-282-122A-32583	Sequence 32583, A
27	369.4	17.1	1722	16 US-10-282-122A-32583	Sequence 32583, A
28	365.4	16.9	1767	16 US-10-282-122A-11945	Sequence 11945, A
29	363.2	16.8	1728	16 US-10-282-122A-14452	Sequence 14452, A
30	361.2	16.7	1716	16 US-10-282-122A-23384	Sequence 23384, A
31	352.4	16.3	1722	16 US-10-282-122A-41795	Sequence 41795, A
32	350.4	16.2	1706	16 US-10-282-122A-19600	Sequence 19600, A
33	345.2	16.0	1806	16 US-10-282-122A-13519	Sequence 13519, A
34	344.8	16.0	1719	9 US-09-815-242-9898	Sequence 9898, Ap
35	344.8	16.0	1719	16 US-10-282-122A-39776	Sequence 39776, A
36	324.4	15.0	1422	9 US-09-965-825-12	Sequence 12, Appl1
37	305.2	14.1	1719	9 US-09-815-242-6012	Sequence 6012, Ap
38	305.2	14.1	1719	13 US-10-096-571-1	Sequence 1, Appl1
39	305.2	14.1	1719	16 US-10-076-416-1	Sequence 1, Appl1
40	305.2	14.1	1719	16 US-10-282-122A-20313	Sequence 20313, A
41	289.8	13.4	1719	16 US-10-282-122A-30639	Sequence 30639, A
42	287.4	13.3	1725	15 US-10-369-493-34030	Sequence 34030, A
43	209	9.7	1140	9 US-09-738-626-2872	Sequence 2872, Ap
44	206.4	9.6	9025608	15 US-10-156-761-1	Sequence 1, Appl1
45	206	9.5	1761	15 US-10-156-761-943	Sequence 943, App

#### ALIGNMENTS

RESULT 1

US-09-965-825-1

Sequence 1, Application US/09965825

Patent No. US20020150999A1

GENERAL INFORMATION:

APPLICANT: DUSCH, Nicole

APPLICANT: THOMAS, Hermann

TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENIC ACID US

FILE REFERENCE: 21354USOX

CURRENT APPLICATION NUMBER: US/09/965, 825

PRIOR APPLICATION NUMBER: DE 10048604.5

PRIOR FILING DATE: 2000-09-30

PRIOR APPLICATION NUMBER: DE 10117085.8

PRIOR FILING DATE: 2001-04-06

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 2160

TYPE: DNA

ORGANISM: Corynebacterium glutamicum

FEATURE:

NAME/KEY: CDS

LOCATION: (327)..(2063)

OTHER INFORMATION:

NAME/KEY: -35 signal

LOCATION: (227)..(232)

OTHER INFORMATION:

NAME/KEY: -10 signal

LOCATION: (256)..(261)

OTHER INFORMATION:

US-09-965-825-1

Query Match 100.0%; Score 2160; DB 9; Length 2160;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAGGCGCATTTCTGAGGTCCTTTTGTGGGTCGCGGTCCTAAATTTGGCCAGTTT 60  
 DB 1 TTGAGGCGCATTTCTGAGGTCCTTTTGTGGGTCGCGGTCCTAAATTTGGCCAGTTT 60

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QY 781 GTGTGTCGAGTGAATGATTCCTGTGATTCCTTAAGAAAGCGAGGTGAACGTAAT 840  
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QY 1021 ATGCGCTGGGTGGTGAAGAGTATCAGACATGAGAAATCGTTGAGGTGGCGATGCTG 1080

DB 1021 ATGCGCTGGGTGGTGAAGAGTATCAGACATGAGAAATCGTTGAGGTGGCGATGCTG 1080

QY 1081 GCGTGTGTTTGAAGGCGCGCGTGGATGCGTCCAAATGAGGGGATTCGTCAATCTAT 1140  
 DB 1081 GCGTGTGTTTGAAGGCGCGCGTGGATGCGTCCAAATGAGGGGATTCGTCAATCTAT 1140

QY 1141 TGGGTACGAAATTCCTTAATCTGATTCCTTCTTAAAGCAACGTTGGCCAGGTGATAT 1200  
 DB 1141 TGGGTACGAAATTCCTTAATCTGATTCCTTCTTAAAGCAACGTTGGCCAGGTGATAT 1200

QY 1201 TCAACGTTGGCGCATTTGTCGACGTAACCAAGTGAATTCGCTGACCGGTGATGTTG 1260  
 DB 1201 TCAACGTTGGCGCATTTGTCGACGTAACCAAGTGAATTCGCTGACCGGTGATGTTG 1260

QY 1261 CTGCAACATCGAAAAATATTTGCTCATGTGAAGAAAAAACAATGCTTCTTCTT 1320  
 DB 1261 CTGCAACATCGAAAAATATTTGCTCATGTGAAGAAAAAACAATGCTTCTTCTT 1320

QY 1321 ATCGATGCTCAAGGCAACAGACGTAAGTGAAGTGGTGGTGAAGAGTACACATA 1380  
 DB 1321 ATCGATGCTCAAGGCAACAGACGTAAGTGAAGTGGTGGTGAAGAGTACACATA 1380

QY 1381 ACGTGGAGAGATGTCCTATTCACCTGAAATACGTTGCTCTATTTGAACGAGCTG 1440  
 DB 1381 ACGTGGAGAGATGTCCTATTCACCTGAAATACGTTGCTCTATTTGAACGAGCTG 1440

QY 1441 CGGATTAAGATGCGGTGTTTACTGTGATACCGGATGACATGTGTGGCATGCGAGT 1500  
 DB 1441 CGGATTAAGATGCGGTGTTTACTGTGATACCGGATGACATGTGTGGCATGCGAGT 1500

QY 1501 ACATGAGAAATCCGAGGGAACGCGCACTTGTGGGTTCAATTCGCGACGCGACGATG 1560  
 DB 1501 ACATGAGAAATCCGAGGGAACGCGCACTTGTGGGTTCAATTCGCGACGCGACGATG 1560

QY 1561 CTAAATGCTGTGCTATGCGATGTTGGTGGCAAAAGTGTGATCGAAACCGGAGGTATG 1620  
 DB 1561 CTAAATGCTGTGCTATGCGATGTTGGTGGCAAAAGTGTGATCGAAACCGGAGGTATG 1620

QY 1621 CGATGTGTGGCGATGTGTGTTGGGATGCTGTGGGTGAAGCTTCTGACCTTAAGCTGC 1680  
 DB 1621 CGATGTGTGGCGATGTGTGTTGGGATGCTGTGGGTGAAGCTTCTGACCTTAAGCTGC 1680

QY 1681 ACCAATCCGCTGAAGGCTGTGGTTTAAACAAGTCTTTTGGGATGTGTAAGTTGG 1740  
 DB 1681 ACCAATCCGCTGAAGGCTGTGGTTTAAACAAGTCTTTTGGGATGTGTAAGTTGG 1740

QY 1741 AGATGCTGTGGAAGGACAGCCAGAAATTTGTAACATGAGAGATGAATTCGACG 1800  
 DB 1741 AGATGCTGTGGAAGGACAGCCAGAAATTTGTAACATGAGAGATGAATTCGACG 1800

QY 1801 AGATTTGCGGCGGCTGCGGATTCAAATTCGATCCGATCCGATCCGAAAGATTCGCG 1860  
 DB 1801 AGATTTGCGGCGGCTGCGGATTCAAATTCGATCCGATCCGATCCGAAAGATTCGCG 1860

QY 1861 AGCAGCTAGCTGAGGCAATGGAATATCTCTGGAACCTGTATCGATGCAATGCTCAAGATC 1920  
 DB 1861 AGCAGCTAGCTGAGGCAATGGAATATCTCTGGAACCTGTATCGATGCAATGCTCAAGATC 1920

QY 1921 CTAATGCGCTGTGATCCACCAACATCACTGTGGAAGAGTCAATGAGATTCAGCAAG 1980  
 DB 1921 CTAATGCGCTGTGATCCACCAACATCACTGTGGAAGAGTCAATGAGATTCAGCAAG 1980

QY 1981 CGGCAACCGGAACCGTCTTGTGTGAGAGATGAGAGCATGATTCATGCGCCGTTTCA 2040  
 DB 1981 CGGCAACCGGAACCGTCTTGTGTGAGAGATGAGAGCATGATTCATGCGCCGTTTCA 2040

QY 2041 ACAATTAAGAAATATCTTACTCATGATGATGATACACCGTGTCTCATTTGACCGGCA 2100  
 DB 2041 ACAATTAAGAAATATCTTACTCATGATGATGATGATACACCGTGTCTCATTTGACCGGCA 2100

QY 2101 GCGTTTACTGCGCAACTTTCCAGATGCGAGCTCAAGCGGCTGACATGAGATTCCTT 2160

Db 2101 GCGCTTAAGTCCCAATTTCCAGAGATGGACCTCAGCGCGGTGCCATGAGATTGCCCT 2160

RESULT 2

US-10-143-856-3

Sequence 3, Application US/10143856

Publication No. US20030109014A1

GENERAL INFORMATION:

APPLICANT: BUREK, KEVIN

APPLICANT: DUNICAN, L.K.

APPLICANT: MCCORMACK, ASHLING

APPLICANT: STRABLETON, CLIONA

APPLICANT: MOCKEL, BETTINA

APPLICANT: THIERBACH, GEORG

TITLE OF INVENTION: Process for the fermentative preparation of

TITLE OF INVENTION: with amplification of the lkt gene

FILE REFERENCE: MAS/021123/282432

CURRENT APPLICATION NUMBER: US/10/143, 856

CURRENT FILING DATE: 2002-05-14

PRIOR APPLICATION NUMBER: 09/986,649

PRIOR FILING DATE: 17-03-2000

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3

LENGTH: 2160

TYPE: DNA

ORGANISM: Corynebacterium glutamicum

FEATURE:

NAME/KEY: CDS

LOCATION: (327)..(2063)

OTHER INFORMATION: poxb

US-10-143-856-3

Query Match 100.0%; Score 2160; DB 15; Length 2160;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGAGCGATTCTGTAGAGTCACTTTTGTGGGTGGGGTCTAAATTTGGCCAGTTT 60

Db 1 TTAGAGCGATTCTGTAGAGTCACTTTTGTGGGTGGGGTCTAAATTTGGCCAGTTT 60

Qy 61 CGAGGCGACGAGACAGGCGGTGCCAGATGTTTAATAGCGATCGGTGGCATCTGTGT 120

Db 61 CGAGGCGACGAGACAGGCGGTGCCAGATGTTTAATAGCGATCGGTGGCATCTGTGT 120

Qy 121 TTGGTTTCAGCGGCTGAACCAACCAAGTCCCGACGACGAGAAATCCCAAAAGT 180

Db 121 TTGGTTTCAGCGGCTGAACCAACCAAGTCCCGACGACGAGAAATCCCAAAAGT 180

Qy 181 GGGGATCCCTGTTGTGATACGAGTACCAACCGGGGCTGAATCCCTGGGCGAGGGGCG 240

Db 181 GGGGATCCCTGTTGTGATACGAGTACCAACCGGGGCTGAATCCCTGGGCGAGGGGCG 240

Qy 241 AAGCGTGGCAACAATGAAATTTAAGACCAATTTGAAGTGCACCAAGTTAGGCAACAC 300

Db 241 AAGCGTGGCAACAATGAAATTTAAGACCAATTTGAAGTGCACCAAGTTAGGCAACAC 300

Qy 301 AATAGCCATAACGTTGAGAGTTCAGATGCGACACAGTACGCAAGAAATTAATTGACA 360

Db 301 AATAGCCATAACGTTGAGAGTTCAGATGCGACACAGTACGCAAGAAATTAATTGACA 360

Qy 361 CTTTGAAGCTCAAGGTTGTAAGGAAATTTATGTTTGGTGGGAGACAGCTTAAATCGA 420

Db 361 CTTTGAAGCTCAAGGTTGTAAGGAAATTTATGTTTGGTGGGAGACAGCTTAAATCGA 420

Qy 421 TCGTGAAGCTCAAGGTTGTAAGGAAATTTATGTTTGGTGGGAGACAGCTTAAATCGA 480

Db 421 TCGTGAAGCTCAAGGTTGTAAGGAAATTTATGTTTGGTGGGAGACAGCTTAAATCGA 480

Qy 481 CCGCGTTTGAAGCGGTTGCGGAATTCGTTGATCACTGGGAGCTGGCAGTATGTCTCTT 540

Db 481 CCGCGTTTGAAGCGGTTGCGGAATTCGTTGATCACTGGGAGCTGGCAGTATGTCTCTT 540

Qy 541 CCGCGTTTGAAGCGGTTGCGGAATTCGTTGATCACTGGGAGCTGGCAGTATGTCTCTT 540

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Db 541 CTTGTGCTCTGGAACAACAACCTGATTCAGGCTCTTTATGATTCGATCGAAATGTG 600

Qy 601 CGAAGGTGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660

Db 601 CGAAGGTGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660

Qy 661 AGGAAAGCAGTCCGGAATTTGTTAAGAAATGCTCTGTTACTGCGAATGATGATGATG 720

Db 661 AGGAAAGCAGTCCGGAATTTGTTAAGAAATGCTCTGTTACTGCGAATGATGATGATG 720

Qy 721 GTGTGAGACAGGTTGAAGCATTTTCATCAGCGATTCAGTCCATGAGCGGTTAAG 780

Db 721 GTGTGAGACAGGTTGAAGCATTTTCATCAGCGATTCAGTCCATGAGCGGTTAAG 780

Qy 781 GTGTGTCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840

Db 781 GTGTGTCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840

Qy 841 ATTCCAAATTCAGTATTTCTTGGGCACTCCTGTTGTTCCGGATCTTACTGAGGCTG 900

Db 841 ATTCCAAATTCAGTATTTCTTGGGCACTCCTGTTGTTCCGGATCTTACTGAGGCTG 900

Qy 901 CAGGCTGTGAGGCGCATTAACAAGCTAAGTCTGACCTTGTTCGGGTCGGGCG 960

Db 901 CAGGCTGTGAGGCGCATTAACAAGCTAAGTCTGACCTTGTTCGGGTCGGGCG 960

Qy 961 TGAAGAAATGCTCGGCGCGAGGTGTTGAGTTGGCGGAGAAATTAATCAACGATCGGGC 1020

Db 961 TGAAGAAATGCTCGGCGCGAGGTGTTGAGTTGGCGGAGAAATTAATCAACGATCGGGC 1020

Qy 1021 ATGCGCTGGGTGTTAAGCAGTATTCAGAGATGAGATTCGTTGAGGTGGGATGTCG 1080

Db 1021 ATGCGCTGGGTGTTAAGCAGTATTCAGAGATGAGATTCGTTGAGGTGGGATGTCG 1080

Qy 1081 GCGTGTGTTAAGCAGTATTCAGAGATGAGATTCGTTGAGGTGGGATGTCG 1140

Db 1081 GCGTGTGTTAAGCAGTATTCAGAGATGAGATTCGTTGAGGTGGGATGTCG 1140

Qy 1141 TGGGATCGAATTCCTTATTCGATTTCTTCTTAAAGCAACGTTGCCAGGTGATA 1200

Db 1141 TGGGATCGAATTCCTTATTCGATTTCTTCTTAAAGCAACGTTGCCAGGTGATA 1200

Qy 1201 TCAACGTTGCGCATTTGTTGATGATGATGATGATGATGATGATGATGATGATGATG 1260

Db 1201 TCAACGTTGCGCATTTGTTGATGATGATGATGATGATGATGATGATGATGATGATG 1260

Qy 1261 CTGCAACATCGAAATTTTGTGCTCATGTGAAGAAATTAATGATCGTTCTCTTG 1320

Db 1261 CTGCAACATCGAAATTTTGTGCTCATGTGAAGAAATTAATGATCGTTCTCTTG 1320

Qy 1321 ATCGATGCTCAAGGCAACAAGCGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1380

Db 1321 ATCGATGCTCAAGGCAACAAGCGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1380

Qy 1381 ACGTCAAGAACATGCTCTTATTCACCTGATTAAGTGAAGTGAAGTGAAGTGAAGTGA 1440

Db 1381 ACGTCAAGAACATGCTCTTATTCACCTGATTAAGTGAAGTGAAGTGAAGTGAAGTGA 1440

Qy 1441 CCGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1500

Db 1441 CCGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1500

Qy 1501 ACATCGAATTCGAGAGGAAACGCGACTTTGTGGTTCAATTCGCGCAAGGACGATG 1560

Db 1501 ACATCGAATTCGAGAGGAAACGCGACTTTGTGGTTCAATTCGCGCAAGGACGATG 1560

Qy 1561 CTATGCTGCTCTCATGCGATTTGTCGCAAGTGTATTCGAAACCGCAGATGATG 1620

Db 1561 CTATGCTGCTCTCATGCGATTTGTCGCAAGTGTATTCGAAACCGCAGATGATG 1620

Qy 1621 CGATGCTGCTCTCATGCGATTTGTCGCAAGTGTATTCGAAACCGCAGATGATG 1680

Db 1621 CGATGCTGCTCTCATGCGATTTGTCGCAAGTGTATTCGAAACCGCAGATGATG 1680

Db 1621 CGATGCTGCGGATGAGTGGGATGCTGCTGGGATGCTTGAACGTTAACTGC 1680  
 Qy 1681 ACCAATTCGCGTGAAGGCGTGTGTGTTAAACAAGTCTTTGGGCAATGTGAAGTTG 1740  
 Db 1681 ACCAATTCGCGTGAAGGCGTGTGTGTTAAACAAGTCTTTGGGCAATGTGAAGTTG 1740  
 Qy 1741 AGATGCTGCGTGAAGGCAAGCCGAAATTTGTACTGATCAATGAGGAAGTGAATTTGCGAG 1800  
 Db 1741 AGATGCTGCGTGAAGGCAAGCCGAAATTTGTACTGATCAATGAGGAAGTGAATTTGCGAG 1800  
 Qy 1801 AGATGCTGCGTGAAGGCGTGTGTGTTAAATTCGTAACGATCAACCGATCGAAGAAAGTTGCGG 1860  
 Db 1801 AGATGCTGCGTGAAGGCGTGTGTGTTAAATTCGTAACGATCAACCGATCGAAGAAAGTTGCGG 1860  
 Qy 1861 AGCAGCTAGCTGAGGATGAGCATTCCTGACCTGTAAGTGAATTCGTAACGATCAACCGATCGAAGAAAGTTGCGG 1920  
 Db 1861 AGCAGCTAGCTGAGGATGAGCATTCCTGACCTGTAAGTGAATTCGTAACGATCAACCGATCGAAGAAAGTTGCGG 1920  
 Qy 1921 CTAAATGCGCTGTGATCCCAACCATCAGTGGGAAAGGATCAATGGGATTCAGCAAG 1980  
 Db 1921 CTAAATGCGCTGTGATCCCAACCATCAGTGGGAAAGGATCAATGGGATTCAGCAAG 1980  
 Qy 1981 CGGCGACCCGAAACCGCTTTGTGTGAGAGATGAGGAGCATGATCGATCGGCGGTTGCA 2040  
 Db 1981 CGGCGACCCGAAACCGCTTTGTGTGAGAGATGAGGAGCATGATCGATCGGCGGTTGCA 2040  
 Qy 2041 ACATAGAGAAATTCCTACTCTCATGATGATGATGATCACTGTGTTCTCATTTGACCGGCA 2100  
 Db 2041 ACATAGAGAAATTCCTACTCTCATGATGATGATGATGATCACTGTGTTCTCATTTGACCGGCA 2100  
 Qy 2101 GGGCTTAATCGGCAACATTTCCAGATGCGAGCTCAGCGCGGTGCCATGATGATGCTT 2160  
 Db 2101 GGGCTTAATCGGCAACATTTCCAGATGCGAGCTCAGCGCGGTGCCATGATGATGCTT 2160

RESULT 3  
 US-10-078-167-4  
 ; Sequence 4, Application US/10078167  
 ; Publication No. US20030119154A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dunican, Rita  
 ; APPLICANT: McCormack, Ashling  
 ; APPLICANT: Stapleton, Cliona  
 ; APPLICANT: Burke, Kevin  
 ; APPLICANT: McKel, Bettina  
 ; TITLE OF INVENTION: Process for the preparation of L-amino acids using  
 ; FILE REFERENCE: 990229 BT-US-B  
 ; CURRENT APPLICATION NUMBER: US/10/078,167  
 ; CURRENT FILING DATE: 2002-02-20  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 4  
 ; LENGTH: 2160  
 ; TYPE: DNA  
 ; ORGANISM: Corynebacterium glutamicum  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (327)..(2063)  
 ; OTHER INFORMATION: poxb  
 US-10-078-167-4

Query Match 100.0%; Score 2160; DB 15; Length 2160;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGAGCGCATTCGTGAGGTCACATTTTGTGGGCGTGGGCTCTAAATTTGGCCGATTTT 60  
 Db 1 TTAGAGCGCATTCGTGAGGTCACATTTTGTGGGCGTGGGCTCTAAATTTGGCCGATTTT 60  
 Qy 61 CGAGGCGACCAAGCGCGTGGCCAGATGTTAAATAGACGATCGTGGGATCTGTGT 120  
 Db 61 CGAGGCGACCAAGCGCGTGGCCAGATGTTAAATAGACGATCGTGGGATCTGTGT 120

Db 61 CGAGGCGACCAAGCGCGTGGCCAGATGTTAAATAGACGATCGTGGGATCTGTGT 120  
 Qy 121 TTGGTTTCGACGGGCTGAAGAACCAACCAAGCTGCCAGCAACAGGAAATCCCAAAAGT 180  
 Db 121 TTGGTTTCGACGGGCTGAAGAACCAACCAAGCTGCCAGCAACAGGAAATCCCAAAAGT 180  
 Qy 181 GGGCATTCCTGTTTGGTACCGAGTACCACCCGGGCTGAAACTCCCTGGCAGGCGGCG 240  
 Db 181 GGGCATTCCTGTTTGGTACCGAGTACCACCCGGGCTGAAACTCCCTGGCAGGCGGCG 240  
 Qy 241 AAGCGTGGCAACATCTGAATTTAAGAGCAATTAAGTCGCAACCAATTTAGGCAAC 300  
 Db 241 AAGCGTGGCAACATCTGAATTTAAGAGCAATTAAGTCGCAACCAATTTAGGCAAC 300  
 Qy 301 AATAGCCATTAAGTTGAGAGGATTCAGATGGCAACAGTACGCAAGAACATTAATGACA 360  
 Db 301 AATAGCCATTAAGTTGAGAGGATTCAGATGGCAACAGTACGCAAGAACATTAATGACA 360  
 Qy 361 CTTTGAAGCTCAAGGTGAGAGCCGAATTTATGTTGTGGGTGACAGCTTAAATCCGA 420  
 Db 361 CTTTGAAGCTCAAGGTGAGAGCCGAATTTATGTTGTGGGTGACAGCTTAAATCCGA 420  
 Qy 421 TCGTGAATCTGTCCGCAATCAGATTAATGATGGGTGACGTTGAAATAGGAAAGG 480  
 Db 421 TCGTGAATCTGTCCGCAATCAGATTAATGATGGGTGACGTTGAAATAGGAAAGG 480  
 Qy 481 CGGCGTTTGAAGCGGTGCGGATGTTGATGATCACTGGGAGCTGACAGTATGTGCTT 540  
 Db 481 CGGCGTTTGAAGCGGTGCGGATGTTGATGATCACTGGGAGCTGACAGTATGTGCTT 540  
 Qy 541 CTTGTGCTCTGAGAAACACAGCTGATTCAGAGGCTTTATGATTCGATGAAATGCTG 600  
 Db 541 CTTGTGCTCTGAGAAACACAGCTGATTCAGAGGCTTTATGATTCGATGAAATGCTG 600  
 Qy 601 CGAAGGTGTGGCAATGCTAGCCATATTCGAGTGCAGATGATGATTCGAGTTCCTCC 660  
 Db 601 CGAAGGTGTGGCAATGCTAGCCATATTCGAGTGCAGATGATGATTCGAGTTCCTCC 660  
 Qy 661 AGGAAACGATCCGAGATTTTGTGTAAGATGCTGTGTTACTGCGAGATGTGATG 720  
 Db 661 AGGAAACGATCCGAGATTTTGTGTAAGATGCTGTGTTACTGCGAGATGTGATG 720  
 Qy 721 GTGTGACAGGAGTGAAGCATTTTGTGATCAGCGGATTCAGTCAACATGCGGAGTAA 780  
 Db 721 GTGTGACAGGAGTGAAGCATTTTGTGATCAGCGGATTCAGTCAACATGCGGAGTAA 780  
 Qy 781 GTGTGCTGCTGTGATGATTCCTGATGATGCTGTAAGAAAGCAGGTGAGGTACTT 840  
 Db 781 GTGTGCTGCTGTGATGATTCCTGATGATGCTGTAAGAAAGCAGGTGAGGTACTT 840  
 Qy 841 ATTCGAATTCACATATTTCTTCTGCGCATCTCTGTGTGTTCCCGGATCTTCTGAGGCTG 900  
 Db 841 ATTCGAATTCACATATTTCTTCTGCGCATCTCTGTGTGTTCCCGGATCTTCTGAGGCTG 900  
 Qy 901 CAGCGCTGTGAGAGCATTTAAACAACGCTAAGTCTGACATTTGTTCTGCGGAGGCG 960  
 Db 901 CAGCGCTGTGAGAGCATTTAAACAACGCTAAGTCTGACATTTGTTCTGCGGAGGCG 960  
 Qy 961 TGAAGAAATGCTCGCGGCGCAGGTGTTGAGTGGCGGAAAGATTAATCAACCGATCGGCG 1020  
 Db 961 TGAAGAAATGCTCGCGGCGCAGGTGTTGAGTGGCGGAAAGATTAATCAACCGATCGGCG 1020  
 Qy 1021 ATGCGCTGGGTGAGTGAAGCATCAATCCAGATAGAAATCCGTTGAGTTCGAGATCTG 1080  
 Db 1021 ATGCGCTGGGTGAGTGAAGCATCAATCCAGATAGAAATCCGTTGAGTTCGAGATCTG 1080  
 Qy 1081 GCTGTGTTGTTACGAGGCTGTGCGTGAATGCGTCAATGAGGCGATCTGCTGATTTCT 1140  
 Db 1081 GCTGTGTTGTTACGAGGCTGTGCGTGAATGCGTCAATGAGGCGATCTGCTGATTTCT 1140  
 Qy 1141 TGGGTACGGAATTTCCCTTATTCGATTTCTTCTTAAAGCAACGTTGCCAGGTGAT 1200  
 Db 1141 TGGGTACGGAATTTCCCTTATTCGATTTCTTCTTAAAGCAACGTTGCCAGGTGAT 1200





QY 721 GTGGTGAAGAGGAGTGAACGATTTTGATCAACGATTCAGTCCACCATGCGGGGTAAAG 780  
 DB 721 GTGGTGAAGAGGAGTGAACGATTTTGATCAACGATTCAGTCCACCATGCGGGGTAAAG 780  
 QY 781 GTGGTGAAGAGGAGTGAACGATTTTGATCAACGATTCAGTCCACCATGCGGGGTAAAG 840  
 DB 781 GTGGTGAAGAGGAGTGAACGATTTTGATCAACGATTCAGTCCACCATGCGGGGTAAAG 840  
 QY 841 ATTCAATTCATATTTCTTCTGAGACTCTGTGTGTTCGCGATTCCTAATGAGGCTG 900  
 DB 841 ATTCAATTCATATTTCTTCTGAGACTCTGTGTGTTCGCGATTCCTAATGAGGCTG 900  
 QY 901 CAGCGCTGTGTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 960  
 DB 901 CAGCGCTGTGTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 960  
 QY 961 TGAAGATCTCGCGGAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1020  
 DB 961 TGAAGATCTCGCGGAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1020  
 QY 1021 ATGCGCTGTGTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1080  
 DB 1021 ATGCGCTGTGTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1080  
 QY 1081 GCGCTGTGTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1140  
 DB 1081 GCGCTGTGTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1140  
 QY 1141 TGGGATCGGATTTCCCTTATTCTGATTTCTTCTTAAAGAAAGAGTTCGCGAGTGAATA 1200  
 DB 1141 TGGGATCGGATTTCCCTTATTCTGATTTCTTCTTAAAGAAAGAGTTCGCGAGTGAATA 1200  
 QY 1201 TCAACGCTGTGTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1260  
 DB 1201 TCAACGCTGTGTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1260  
 QY 1261 CTGCAACAATCGAATAATTTTGGCTCATGTGAAGAAAGAAAGAGTTCGCGAGTGAATA 1320  
 DB 1261 CTGCAACAATCGAATAATTTTGGCTCATGTGAAGAAAGAAAGAGTTCGCGAGTGAATA 1320  
 QY 1321 ATCGGATCTCAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1380  
 DB 1321 ATCGGATCTCAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1380  
 QY 1381 ACGTGAAGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1440  
 DB 1381 ACGTGAAGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1440  
 QY 1441 CGGATTAAGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1500  
 DB 1441 CGGATTAAGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1500  
 QY 1501 ACATCGGAATTCGAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1560  
 DB 1501 ACATCGGAATTCGAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1560  
 QY 1561 CTATGCTGTGTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1620  
 DB 1561 CTATGCTGTGTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1620  
 QY 1621 CGATGCTGTGTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1680  
 DB 1621 CGATGCTGTGTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1680  
 QY 1681 ACCAATCTTCGCTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1740  
 DB 1681 ACCAATCTTCGCTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1740  
 QY 1741 AGATGCTGTGTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1800  
 DB 1741 AGATGCTGTGTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1800  
 QY 1801 AGATGCTGTGTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1860  
 DB 1801 AGATGCTGTGTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1860

DB 1801 AGATGCTGTGTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1860  
 QY 1861 AGCAGTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1920  
 DB 1861 AGCAGTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1920  
 QY 1921 CTATGCTGTGTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1980  
 DB 1921 CTATGCTGTGTGAAGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 1980  
 QY 1981 CCGGCAACCGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 2040  
 DB 1981 CCGGCAACCGGAGTGAACGATTCAGTCCACCATGCGGGGTAAAG 2040  
 QY 2041 ACATTAAGAAATTTCTTCTGAGACTCTGTGTGTTCGCGATTCCTAATGAGGCTG 2100  
 DB 2041 ACATTAAGAAATTTCTTCTGAGACTCTGTGTGTTCGCGATTCCTAATGAGGCTG 2100  
 QY 2101 GCGCTTAACCTGCAACATTTCCAGATTCAGTCCACCATGCGGGGTAAAG 2160  
 DB 2101 GCGCTTAACCTGCAACATTTCCAGATTCAGTCCACCATGCGGGGTAAAG 2160

RESULT 5  
 US-10-091-342-4  
 ; Sequence 4, Application US/10091342  
 ; Publication No. US20030199045A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Degussa AG  
 ; APPLICANT: National University of Ireland, Galway  
 ; APPLICANT: Forschungszentrum Jülich GmbH  
 ; TITLE OF INVENTION: Process for the fermentative preparation of L-Amino Acids with  
 ; FILE REFERENCE: 9902395P  
 ; CURRENT APPLICATION NUMBER: US/10/091,342  
 ; CURRENT FILING DATE: 2002-03-06  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 4  
 ; LENGTH: 2160  
 ; TYPE: DNA  
 ; ORGANISM: Corynebacterium glutamicum  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (327)..(2063)  
 ; OTHER INFORMATION: poxb  
 US-10-091-342-4

Query Match 100.0%; Score 2160; DB 15; Length 2160;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTAAGAGCGATTCGTGAGTCACTTTTGTGGGGTGGGGTCTAAATTTGGCCAGTTT 60  
 DB 1 TTAAGAGCGATTCGTGAGTCACTTTTGTGGGGTGGGGTCTAAATTTGGCCAGTTT 60  
 QY 61 CGAGGCGACAGAGGCGGCCAGAGTGTAAATTAAGGCGATCGGTGGGCACTGTGT 120  
 DB 61 CGAGGCGACAGAGGCGGCCAGAGTGTAAATTAAGGCGATCGGTGGGCACTGTGT 120  
 QY 121 TTGGTTTGAAGGCGCTGAAACCAACAGACTGCGGCAAGAGGAAATCCCAAAAGT 180  
 DB 121 TTGGTTTGAAGGCGCTGAAACCAACAGACTGCGGCAAGAGGAAATCCCAAAAGT 180  
 QY 181 GGGATATCCCTGTTTGTGATCCGAGTACCCACCGGGCTGAAATCCCTGCGAGCGGG 240  
 DB 181 GGGATATCCCTGTTTGTGATCCGAGTACCCACCGGGCTGAAATCCCTGCGAGCGGG 240  
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 DB 241 AAGGTGGCAACAATCGGAATTTAAGAGCAATTAAGTCCGACCAAGTTAGGCAAC 300



QY 301 AATAGCCATTAAGAGAGTTCAATGCGACACAGCTACGCGAACAATTAATTGACA 360  
 DB 301 AATAGCCATTAAGAGAGTTCAATGCGACACAGCTACGCGAACAATTAATTGACA 360  
 QY 361 CTTTGGAAAGTCAAGGTGTGAAGCGAATTTATGTTTGGTGGTGAACAGCTTAATCCGA 420  
 DB 361 CTTTGGAAAGTCAAGGTGTGAAGCGAATTTATGTTTGGTGGTGAACAGCTTAATCCGA 420  
 QY 421 TCGTGAATGCTGCGGCAATCAGATATTGATGAGGTGCGTTCGAAATGAGGAACGG 480  
 DB 421 TCGTGAATGCTGCGGCAATCAGATATTGATGAGGTGCGTTCGAAATGAGGAACGG 480  
 QY 481 CCGCGTTTGGCAGCGGTGCGAATTCGTGATCACTGGGAGCTGGCAGTATGTGCTT 540  
 DB 481 CCGCGTTTGGCAGCGGTGCGAATTCGTGATCACTGGGAGCTGGCAGTATGTGCTT 540  
 QY 541 CTTTGGTCTTGGAAACACACCTGATTCAGGGTCTTTATGATTCGATCGAAATGTG 600  
 DB 541 CTTTGGTCTTGGAAACACACCTGATTCAGGGTCTTTATGATTCGATCGAAATGTG 600  
 QY 601 CGAAGGTGTTGGCAGCTAGGCAATTCGAGTGGCCAGATTGTTGACGTTCTTCC 660  
 DB 601 CGAAGGTGTTGGCAGCTAGGCAATTCGAGTGGCCAGATTGTTGACGTTCTTCC 660  
 QY 661 AGGAAACGATCCGAGATTTTGTAAAGAAATGCTGTTTCTGCGAATGTGTAATG 720  
 DB 661 AGGAAACGATCCGAGATTTTGTAAAGAAATGCTGTTTCTGCGAATGTGTAATG 720  
 QY 721 GTGTGAGACAGGTGAAACGATTTTGTATCAAGGATTCAGTCCATGAGCGGTAAAG 780  
 DB 721 GTGTGAGACAGGTGAAACGATTTTGTATCAAGGATTCAGTCCATGAGCGGTAAAG 780  
 QY 781 GTGTGTCGAGGTGATGATTCCTGTTGATTCGTTAAAGAAACGAGGTGAAGCTT 840  
 DB 781 GTGTGTCGAGGTGATGATTCCTGTTGATTCGTTAAAGAAACGAGGTGAAGCTT 840  
 QY 841 ATTCCAATTCATATTTCTTCTGAGCACTCTGTGTTCCGCGATCTACTAGAGCTG 900  
 DB 841 ATTCCAATTCATATTTCTTCTGAGCACTCTGTGTTCCGCGATCTACTAGAGCTG 900  
 QY 901 CAGCGCTGTGAGAGCGATTAACAAGCTTAAGTCTGCTCACTTGTCTGCGGTGCGGCG 960  
 DB 901 CAGCGCTGTGAGAGCGATTAACAAGCTTAAGTCTGCTCACTTGTCTGCGGTGCGGCG 960  
 QY 961 TGAAGAATGCTCGCGCGCAGGTGTGAAGTTGGCGGAAGATTAAATCAACCATCGGCG 1020  
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 DB 1021 ATGCGCTGAGGTGAAGCAGTATCAAGCATGAGATCCGTTTGAAGTGGCAGTGTCTG 1080  
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 DB 1141 TGGGTACGAGATTTCCCTTATCTGATTTCTTCTTAAAGCAACGTTGCCAGGTGATA 1200  
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 DB 1261 CTGCAACAATCGAAAATATTTTGGCTCATGTGAAGAAAAACAAGATGTTCTCTCTTGG 1320  
 QY 1321 ATGGAATGCTCAAGGCAACAGAGCTGAAGTTGAGTGGTGGTGAAGAGTACACACATA 1380  
 DB 1321 ATGGAATGCTCAAGGCAACAGAGCTGAAGTTGAGTGGTGGTGAAGAGTACACACATA 1380  
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DB 1381 AGGTGGAAGAGATGTGCTTATCACCTGTAATAGTTGCTCTATTTGAAGAGCTGG 1440  
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 DB 1441 CCGAATAAGATGGGTGTTTACGTGATACCGGCAATGTGATGTGCAATCGGAGT 1500  
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 DB 1501 ACATCGAATTCGAGAGGAACCGCGACTTGTGAGTTCAATCCGCAAGCGACGATGG 1560  
 QY 1561 CTATGCGTTGCTCATGCGATTTGTGCGCAAAAGTTGATCGAAACCGCAAGTATCG 1620  
 DB 1561 CTATGCGTTGCTCATGCGATTTGTGCGCAAAAGTTGATCGAAACCGCAAGTATCG 1620  
 QY 1621 CGATGTGCGAATGTGTTGAGTTGGGATGTGCTGCTGGGTGAGCTTGAACGTTAAGCTGC 1680  
 DB 1621 CGATGTGCGAATGTGTTGAGTTGGGATGTGCTGCTGGGTGAGCTTGAACGTTAAGCTGC 1680  
 QY 1681 ACCAATTCGCGTGAAGCTGTGTTTAAACAAGTTCTTTGGCAGTGTGAAGTTGG 1740  
 DB 1681 ACCAATTCGCGTGAAGCTGTGTTTAAACAAGTTCTTTGGCAGTGTGAAGTTGG 1740  
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 DB 1741 AGATGCTGTGAGAGGACACCGAATTTGTAATGATGAGAAAGTGAATTTGCGAG 1800  
 QY 1801 AGATGGGCGGCTGGCGGTGATCAATCGTGAAGCATACCGATCCGAAAGTTGCGG 1860  
 DB 1801 AGATGGGCGGCTGGCGGTGATCAATCGTGAAGCATACCGATCCGAAAGTTGCGG 1860  
 QY 1861 AGAGCTAGCTGAGGCAATTTGGCATTCCTGACCTGATGATGATGATGATGATGATG 1920  
 DB 1861 AGAGCTAGCTGAGGCAATTTGGCATTCCTGACCTGATGATGATGATGATGATGATG 1920  
 QY 1921 CTATGCGTGTGATCCCAACCAATCAAGTGAACAGGTCAATGGAATTCAGCAAGG 1980  
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 QY 1981 CCGCACCAGCAACCGTCTTTGTGAGAGATGAGAGGATGATGATGATGATGATGATG 2040  
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 DB 2041 ACATTAAGAAATATTCCTACTCCATGATGATGATGATGATGATGATGATGATGATG 2100  
 QY 2101 GCGCTTAATCCCAACATTTCCAGAGTGGCAGCTCAGCGGTGCCATGAGATGGCTT 2160  
 DB 2101 GCGCTTAATCCCAACATTTCCAGAGTGGCAGCTCAGCGGTGCCATGAGATGGCTT 2160

RESULT 6  
 US-10-686-736-4  
 ; Sequence 4, Application US/10686736  
 ; Publication No. US20040063181A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dunican, Rita  
 ; APPLICANT: McCormack, Ashling  
 ; APPLICANT: Stapleton, Cliona  
 ; APPLICANT: Burke, Kevin  
 ; APPLICANT: McKel, Bettina  
 ; TITLE OF INVENTION: Process for the preparation of L-amino acids using  
 ; a gene encoding 6-Phosphogluconate Dehydrogenase  
 ; FILE REFERENCE: 990229 BT-US-B  
 ; CURRENT APPLICATION NUMBER: US/10/686,736  
 ; PRIOR APPLICATION NUMBER: US/10/078,167A  
 ; PRIOR FILING DATE: 2002-02-22  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 4  
 ; LENGTH: 2160

TYPE: DNA  
ORGANISM: Corynebacterium glutamicum  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (327)..(2063)  
OTHER INFORMATION: poxb  
US-10-686-736-4

Query Match 100.0%; Score 2160; DB 16; Length 2160;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TTAAGGCGATTCGTGTAGGTCACTTTTGTGGGGTCCGAGCTAAATTTGGCCAGTTT 60
QY 61 CGAGCGACGACGAGCGGTCGCCAAGTGTAAATAGCGATCGGTGGGCACTGTGT 120
DB 61 CGAGCGACGACGAGCGGTCGCCAAGTGTAAATAGCGATCGGTGGGCACTGTGT 120
QY 121 TTGGTTTCGACGGGCTGTAACCAACAGACTGCCAGCAACAGCGAAATCCCAAAAGT 180
DB 121 TTGGTTTCGACGGGCTGTAACCAACAGACTGCCAGCAACAGCGAAATCCCAAAAGT 180
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DB 241 AAGCGTGGCAACAATGGAATTTAAGACCAATTTGAAGTCCGACCAAGTTAGGCAAC 300
QY 301 AATAGCCATAACCTTTAGAGAGTTCAATGACACACAGCTACGAGAACATTAATTGACA 360
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QY 421 TCGTGATGCTGTCCGCAATCAGATTTAGTGGGTGACAGCTTCAAAATGAGAGACGG 480
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DB 601 CGAAGGTGTGGCCATCGCTAGCCATATTCAGAGTCCGAGATGCTGACAGTTCTTCC 660
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DB 781 GTGTGTCTGTGTATGATTTCTGTGTATATGCTTAAGAGAGAGCAGAGTGAACGTA 840
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DB 841 ATTCCAAATCCCAATTTCTTCTGAGCACTCTGTGTGTTCGCGATCTTACTGAGGCTG 900
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DB 1021 ATGCGCTGGGTGTGAAGCAGTACATCCAGATGAGAATCCGTTTGAAGTCCGATGCTG 1080
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DB 1141 TGGGTACGGAATTCCTTATTTCTGATTTCTTCTTAAGACAAAGTGTGCCAGTGGATA 1200
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DB 1321 ATCGATGCTCAAGGACACGAGCGTAAAGTGAAGTCCGTGTGAGACGTAACACATA 1380
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DB 1381 ACGTGAAGAGCATGCTTACCTTAACTGCTGCTTATTTTGAACGAGCTGG 1440
QY 1441 CGGATTAAGATGCGGTGTTTACTGTGATACCGGATGCAATGTGGATGCGAGGT 1500
DB 1441 CGGATTAAGATGCGGTGTTTACTGTGATACCGGATGCAATGTGGATGCGAGGT 1500
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DB 1501 ACATGAAGATTCGGAAGGAAACGCGCACTTTGGGTTCAATTCGCAACGCGACGATG 1560
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DB 1561 CTAATGCTGCTCATATCGATGAGTGGCGAAAGTGTGTGAACGCGCAGAGTATCG 1620
QY 1621 CGATGTGTGGGATGTGTTGGCATGCTGTGGTGAAGCTTCTGACCTTAAAGCTGC 1680
DB 1621 CGATGTGTGGGATGTGTTGGCATGCTGTGGTGAAGCTTCTGACCTTAAAGCTGC 1680
QY 1681 ACCAATTCGCTGAAGGCTGTGGTGTAAACAAGTCTTTTGGGATGATGTAAGTTGG 1740
DB 1681 ACCAATTCGCTGAAGGCTGTGGTGTAAACAAGTCTTTTGGGATGATGTAAGTTGG 1740
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DB 1741 AGATGCTGTGAGAGGACAGCAGAAATTTGTACTGACATGAGAGAGTAATTTGGCAG 1800
QY 1801 AGATTTGGGCGGCTGCGGATTAATCGGTACGATCACCGATCCGAGAAAGTTGCG 1860
DB 1801 AGATTTGGGCGGCTGCGGATTAATCGGTACGATCACCGATCCGAGAAAGTTGCG 1860
QY 1861 AGCAGTAGCTGAGGACATTTGGCAATCTGAGACCTGTACTGATGATTCGATACGATC 1920
DB 1861 AGCAGTAGCTGAGGACATTTGGCAATCTGAGACCTGTACTGATGATTCGATACGATC 1920
QY 1921 CTAATGCGCTGTGATCCCAACAATCACTGTGGAACAGTCAATGGATTCAGCAAG 1980
DB 1921 CTAATGCGCTGTGATCCCAACAATCACTGTGGAACAGTCAATGGATTCAGCAAG 1980
QY 1981 CAGCACCAGAACCGTCTTTGTGTGAGAGATGAGAGATGATGATCTGGCCGTTGCA 2040
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[illegible]

Db	2777870	GGAAAGAAATGCTCGCGCGCAGGATGTTGGAGTTGGCGGAGAAATTAATCAACCCATCCGGC	2777811
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Db	2777810	ATGCGCTGGTGTGTAAGCATCATCCAGCATGAGAAATCCGTTTGAAGTCGACATGTC	2777511
Qy	1081	GCCTGCTTGGTTACGCGCGCTGCGGTGATGCGTCCAAATGAGCCGATCTGCTGATTTCTAT	1140
Db	2777750	GCCTGCTTGGTTACGCGCGCTGCGGTGATGCGTCCAAATGAGCCGATCTGCTGATTTCTAT	2776911
Qy	1141	TGGGTACGGATTTTCCCTTATTTCTGATTTCTTCTTAAAGCAACGTTGCCAGGTGATA	1200
Db	2777650	TGGGTACGGATTTTCCCTTATTTCTGATTTCTTCTTAAAGCAACGTTGCCAGGTGATA	2777631
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Db	2777630	TCAACGGTGCACATTTGTCGACGTACCAACGGTGAAGTATCCGGTGAACGGGTATGTC	2777571
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Db	2777570	CTGCACCAATGGAAAATATTTTGTCTCATGTGAAAGAAAAACAGATGTTCTTCTTCTG	2777511
Qy	1321	ATCGGATCTCAAGGCACACAGCGCTAAGTTAGCTCGGTGTGAGACGTACACATTA	1380
Db	2777510	ATCGGATCTCAAGGCACACAGCGCTAAGTTAGCTCGGTGTGAGACGTACACATTA	2777451
Qy	1381	ACGTGGAAGACATGTGCTCTATTCAACCTTGATACGTTGCTCTATTTTGAACGAGCTG	1440
Db	2777450	ACGTGGAAGACATGTGCTCTATTCAACCTTGATACGTTGCTCTATTTTGAACGAGCTG	2777391
Qy	1441	CGGATTAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCATGTGTGCATTCGAGCT	1500
Db	2777390	CGGATTAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCATGTGTGCATTCGAGCT	2777331
Qy	1501	ACATGGAATATCCGGAGGGAAACGGCGACTTTGTGGTTCAATTCGGCACGGCACGATGG	1560
Db	2777330	ACATGGAATATCCGGAGGGAAACGGCGACTTTGTGGTTCAATTCGGCACGGCACGATGG	2777271
Qy	1561	CTAATGCGTTGCTTCATCATGCGATGTGTGCGCAAGTGTGATCGAAACCGCACGGTGAATG	1620
Db	2777270	CTAATGCGTTGCTTCATCATGCGATGTGTGCGCAAGTGTGATCGAAACCGCACGGTGAATG	2777211
Qy	1621	CGATGTGTGCGATGTGTGTTGGGCATGCTGCTGGGTGAACCTTCTGACGTTAAGCTGC	1680
Db	2777210	CGATGTGTGCGATGTGTGTTGGGCATGCTGCTGGGTGAACCTTCTGACGTTAAGCTGC	2777151
Qy	1681	ACCAACTTCCGCTGAAGGCTGTGTGTGTTTAAACAAGTTCTTTGGGCAATGTGTAAGTTGG	1740
Db	2777150	ACCAACTTCCGCTGAAGGCTGTGTGTGTTTAAACAAGTTCTTTGGGCAATGTGTAAGTTGG	2777091
Qy	1741	AGATGCTGTGGAAGGACAGCCAGAAATTTGGTACTGACCATGAGGAAAGTGAATTTCCGAG	1800
Db	2777090	AGATGCTGTGGAAGGACAGCCAGAAATTTGGTACTGACCATGAGGAAAGTGAATTTCCGAG	2777031
Qy	1801	AGATTGCGGCGGCTGCGGGTATCAAATCGTATCGCATCACCGATCCGAAGAAATTTCCGC	1860
Db	2777030	AGATTGCGGCGGCTGCGGGTATCAAATCGTATCGCATCACCGATCCGAAGAAATTTCCGC	2776971
Qy	1861	AGCAGCTATGCTGAAGGCATTTGGCATATCTCTGACCTGTATCTGATGTGATATCTGCACGATC	1920
Db	2776970	AGCAGCTATGCTGAAGGCATTTGGCATATCTCTGACCTGTATCTGATGTGATATCTGCACGATC	2776911
Qy	1921	CTAATGCGCTGTGATCCCAACCAACATCATGTTGGGAAACAGGTATGAGGAAATTTGACAGG	1980
Db	2776910	CTAATGCGCTGTGATCCCAACCAACATCATGTTGGGAAACAGGTATGAGGAAATTTGACAGG	2776851
Qy	1981	CGGCCACCCGAACCGTCTTTTGTGTGAGAGTAGAGCGATGATCTGCGCCGTTTCSA	2040
Db	2776850	CGGCCACCCGAACCGTCTTTTGTGTGAGAGTAGAGCGATGATCTGCGCCGTTTCSA	2776791
Qy	2041	ACATTAAGGAATATTTCTCATCTCAATGATATTTGATATCACCTGCTGTCTTCATTTGACCGCGA	2100
Db	2776790	ACATTAAGGAATATTTCTCATCTCAATGATATTTGATATCACCTGCTGTCTTCATTTGACCGCGA	2776731

QY	2101	GGCGTTAACTGCGCAACATTTCCAGAGATGCGAGCGCGGTGCCATGAGATTGCGCT	2160
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US-10-781-014-85			
; Sequence 85, Application US/10781014			
; Publication No. US20040180408A1			
; GENERAL INFORMATION:			
; APPLICANT: Pompejus, Markus			
; APPLICANT: Kroege, Burkhard			
; APPLICANT: Schröder, Hartwig			
; APPLICANT: Zeidler, Oskar			
; APPLICANT: Haberhauser, Gregor			
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS			
; TITLE OF INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY			
; TITLE OF INVENTION: PRODUCTION			
; FILE REFERENCE: BGI-126CPN			
; CURRENT APPLICATION NUMBER: US/10/781,014			
; CURRENT FILING DATE: 2004-02-17			
; PRIOR APPLICATION NUMBER: US 09/602,740			
; PRIOR FILING DATE: 2000-06-23			
; PRIOR APPLICATION NUMBER: 60/141,031			
; PRIOR FILING DATE: 1999-06-25			
; PRIOR APPLICATION NUMBER: 60/143,208			
; PRIOR FILING DATE: 1999-07-09			
; PRIOR APPLICATION NUMBER: 60/151,572			
; PRIOR FILING DATE: 1999-08-31			
; PRIOR APPLICATION NUMBER: DE 19931412.8			
; PRIOR FILING DATE: 1999-07-08			
; PRIOR APPLICATION NUMBER: DE 19931413.6			
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; PRIOR FILING DATE: 1999-07-08			
; PRIOR APPLICATION NUMBER: DE 19931420.9			
; PRIOR FILING DATE: 1999-07-08			
; PRIOR APPLICATION NUMBER: DE 19931424.1			
; PRIOR FILING DATE: 1999-07-08			
; PRIOR APPLICATION NUMBER: DE 19931428.4			
; PRIOR FILING DATE: 1999-07-08			
; Remaining Prior Application data removed - See File Wrapper or PALM.			
; NUMBER OF SEQ ID NOS: 784			
; SEQ ID NO 85			
; LENGTH: 1860			
; TYPE: DNA			
; ORGANISM: Corynebacterium glutamicum			
; FEATURES:			
; NAME/KEY: CDS			
; LOCATION: (101)..(1837)			
; OTHER INFORMATION: KX000635			
US-10-781-014-85			
Query Match 86.1%; Score 1860; DB 17; Length 1860;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1860; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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QY	287	AAGTTAGGCAACAATTAGCATTAAGCTTGAAGAGGTCAGATGGCACACAGCTACGAGA	346
Db	61	AAGTTAGGCAACAATTAGCATTAAGCTTGAAGAGGTCAGATGGCACACAGCTACGAGA	120
QY	347	ACAATTAATGACACTTTGGAAGCTCAAGGTGTAACGCAATTTATGTTTGTTGTTG	406
Db	121	ACAATTAATGACACTTTGGAAGCTCAAGGTGTAACGCAATTTATGTTTGTTGTTG	180
QY	407	CAGCTTAATTCATGCTGTGATGCTGTCCGCAATCATGATATTGATGTTGGTGCACGTTGC	466
Db	181	CAGCTTAATTCATGCTGTGATGCTGTCCGCAATCATGATATTGATGTTGGTGCACGTTGC	240

QY 467 AAATGAGAAAGCGCGCGTTTGACGCGGTGGGAATGTTGATGACATGCGGAGCTGGC 526  
 DB 241 AAATGAGAAAGCGCGCGTTTGACGCGGTGGGAATGTTGATGACATGCGGAGCTGGC 300  
 QY 527 AGTATGCTGCTCTTCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 586  
 DB 301 AGTATGCTGCTCTTCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
 QY 587 GCATGAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 646  
 DB 361 GCATGAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
 QY 647 TTGACGCTTCTTCCAGAAACGATCCGAGATTTTGTGTTAGAAATGCTGCTGCTGCTGCT 706  
 DB 421 TTGACGCTTCTTCCAGAAACGATCCGAGATTTTGTGTTAGAAATGCTGCTGCTGCTGCT 480  
 QY 707 CGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 766  
 DB 481 CGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
 QY 767 CATGCGGAGTAAAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 826  
 DB 541 CATGCGGAGTAAAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
 QY 827 AGGTGACGCTTCTTCCAGAAACGATCCGAGATTTTGTGTTAGAAATGCTGCTGCTGCTGCT 886  
 DB 601 AGGTGACGCTTCTTCCAGAAACGATCCGAGATTTTGTGTTAGAAATGCTGCTGCTGCTGCT 660  
 QY 887 TCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 946  
 DB 661 TCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
 QY 947 CTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1006  
 DB 721 CTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
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 DB 781 ATCCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
 QY 1067 GGTGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1126  
 DB 841 GGTGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
 QY 1127 TCTGCTGATTTCTATTTGGGATGCGATTTCCCTTATTTCTGATTTCTTCTTAAAGCAACGT 1186  
 DB 901 TCTGCTGATTTCTATTTGGGATGCGATTTCCCTTATTTCTGATTTCTTCTTAAAGCAACGT 960  
 QY 1187 TGCCAGAGTGGATTCACACGCTGCGGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1246  
 DB 961 TGCCAGAGTGGATTCACACGCTGCGGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
 QY 1247 GACCGGATGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1306  
 DB 1021 GACCGGATGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
 QY 1307 TCGTCTCTTCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1366  
 DB 1081 TCGTCTCTTCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
 QY 1367 GACGTACACATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1426  
 DB 1141 GACGTACACATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200  
 QY 1427 TTTTGAACGAGTGGCGATTAAGATGCGGTGTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1486  
 DB 1201 TTTTGAACGAGTGGCGATTAAGATGCGGTGTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260  
 QY 1487 GTGGCATGAGGATTCATGAGATTCGGAAGGAAACGCGCATTTTGTGGTTCATTCG 1546  
 DB 1261 GTGGCATGAGGATTCATGAGATTCGGAAGGAAACGCGCATTTTGTGGTTCATTCG 1320

QY 1547 CCACGGACAGATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1606  
 DB 1321 CCACGGACAGATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380  
 QY 1607 CCGCAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1666  
 DB 1381 CCGCAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440  
 QY 1667 GACCGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1726  
 DB 1441 GACCGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
 QY 1727 CATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1786  
 DB 1501 CATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560  
 QY 1787 AGTGAATTTGACAGATTTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1846  
 DB 1561 AGTGAATTTGACAGATTTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620  
 QY 1847 GAAGAAAGTTGCGGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1906  
 DB 1621 GAAGAAAGTTGCGGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680  
 QY 1907 TATGCTGAGGATTTCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1966  
 DB 1681 TATGCTGAGGATTTCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
 QY 1967 GGGATTCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2026  
 DB 1741 GGGATTCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800  
 QY 2027 TCTGCGGCTTGTGAACATTAAGATTTCTTCTGATGATGATGATGATGATGATGATGATGATGAT 2086  
 DB 1801 TCTGCGGCTTGTGAACATTAAGATTTCTTCTGATGATGATGATGATGATGATGATGATGATGAT 1860

## RESULT 10

US-09-738-626-2873  
 ; Sequence 2873, Application US/09738626  
 ; Publication No. US20020197605A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NAKAGAMA, SATOSHI  
 ; APPLICANT: MIZOGUCHI, HIROSHI  
 ; APPLICANT: ANDO, SEIKO  
 ; APPLICANT: HAYASHI, MIKIRO  
 ; APPLICANT: OCHIAI, KEIKO  
 ; APPLICANT: YOKOI, HARUHIKO  
 ; APPLICANT: TATEISHI, NAOKO  
 ; APPLICANT: SENOH, AKIHIRO  
 ; APPLICANT: IKEDA, MASATO  
 ; APPLICANT: OZAKI, AKIO  
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 ; FILE REFERENCE: 249-125  
 ; CURRENT APPLICATION NUMBER: US/09/738, 626  
 ; PRIOR FILING DATE: 2000-12-18  
 ; PRIOR APPLICATION NUMBER: JP 99/377484  
 ; PRIOR FILING DATE: 1999-12-16  
 ; PRIOR APPLICATION NUMBER: JP 00/159162  
 ; PRIOR FILING DATE: 2000-04-07  
 ; PRIOR APPLICATION NUMBER: JP 00/280988  
 ; PRIOR FILING DATE: 2000-08-03  
 ; NUMBER OF SEQ ID NOS: 7059  
 ; SOFTWARE: PatentIn ver. 3.0  
 ; SEQ ID NO 2873  
 ; LENGTH: 1737  
 ; TYPE: DNA  
 ; ORGANISM: *Corynebacterium glutamicum*

Query Match 80.4%; Score 1737; DB 9; Length 1737;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1737; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 327 ATGGCAACAGCTACGAGAACTTAATTGACCTTGGAAAGCTCAAGTGTGAAGGA 386  
 Db 1 ATGGCAACAGCTACGAGAACTTAATTGACCTTGGAAAGCTCAAGTGTGAAGGA 60  
 QY 387 ATTTATGTTTGGTGGTGAAGAGCTTAATCCGATCGTGATGCTGTCCGCAATCAGAT 446  
 Db 61 ATTTATGTTTGGTGGTGAAGAGCTTAATCCGATCGTGATGCTGTCCGCAATCAGAT 120  
 QY 447 ATTAGAGGTGGTGAAGCTTGAATGAGGAAGGAGGAGGCTTGGAGCCGAGGCAATCG 506  
 Db 121 ATTAGAGGTGGTGAAGCTTGAATGAGGAAGGAGGAGGCTTGGAGCCGAGGCAATCG 180  
 QY 507 TTGATCACTGGGAGCTGGAGATAGTGTCTCTTGGTCTCTGAAACAACAACCTG 566  
 Db 181 TTGATCACTGGGAGCTGGAGATAGTGTCTCTTGGTCTCTGAAACAACAACCTG 240  
 QY 567 ATTGAGGTCTTTATGATTCGATCGAATGATGCGAAGGTGGTGGCCATCGTAGCCAT 626  
 Db 241 ATTGAGGTCTTTATGATTCGATCGAATGATGCGAAGGTGGTGGCCATCGTAGCCAT 300  
 QY 627 ATTCGAGTCCGAGATTTGGTTCAGCTTCCAGAGAAAGCAATCCGAGATTTGTTT 686  
 Db 301 ATTCGAGTCCGAGATTTGGTTCAGCTTCCAGAGAAAGCAATCCGAGATTTGTTT 360  
 QY 687 AAGGATGCTGTGGTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 746  
 Db 361 AAGGATGCTGTGGTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 420  
 QY 747 CATGACGAGATTCAGTCCATCATGAGGAGTGAAGTGTGCTGGTGTGATGATTCCTG 806  
 Db 421 CATGACGAGATTCAGTCCATCATGAGGAGTGAAGTGTGCTGGTGTGATGATTCCTG 480  
 QY 807 GATATGCTTAAGGAAGAGAGAGTGAAGTGAATTCATTCATTCATTCATTCATTCATTC 866  
 Db 481 GATATGCTTAAGGAAGAGAGTGAAGTGAATTCATTCATTCATTCATTCATTCATTC 540  
 QY 867 ACTCTGTGTGTTCCTGGATCTACTGAGGCTGAGGCTGATGAGGAGCAATTAACAC 926  
 Db 541 ACTCTGTGTGTTCCTGGATCTACTGAGGCTGAGGCTGATGAGGAGCAATTAACAC 600  
 QY 927 GCTAAGTCTGTCACTTGTCTGTGGTGGTGAAGTGTGCTGGTGTGATGATTCCTG 986  
 Db 601 GCTAAGTCTGTCACTTGTCTGTGGTGGTGAAGTGTGCTGGTGTGATGATTCCTG 660  
 QY 987 GAGTGGCGGAGAAATTAATCAACGATCGGAGATGCTGGTGGTGAAGTGAATTCCTG 1046  
 Db 661 GAGTGGCGGAGAAATTAATCAACGATCGGAGATGCTGGTGGTGAAGTGAATTCCTG 720  
 QY 1047 CAGATGAGATCCGTTGAGGTGGAGATGCTGGGCTGCTGTTGTTACGGGCTGGGCTG 1106  
 Db 721 CAGATGAGATCCGTTGAGGTGGAGATGCTGGGCTGCTGTTGTTACGGGCTGGGCTG 780  
 QY 1107 GATGCGTCCAATGAGGAGATCTGCTGATTCATTTGGGTAAGATTCCTTATTCGAT 1166  
 Db 781 GATGCGTCCAATGAGGAGATCTGCTGATTCATTTGGGTAAGATTCCTTATTCGAT 840  
 QY 1167 TTCTCTTCTTAAAGCAAGTTCCTGCTGATGATGATGATGATGATGATGATGATGATG 1226  
 Db 841 TTCTCTTCTTAAAGCAAGTTCCTGCTGATGATGATGATGATGATGATGATGATGATG 900  
 QY 1227 ACCACGAGTGAAGTTCGAGTGAAGGAGTGGCTGCAACATTCGAAATTTTTCCT 1286  
 Db 901 ACCACGAGTGAAGTTCGAGTGAAGGAGTGGCTGCAACATTCGAAATTTTTCCT 960  
 QY 1287 CATGTGAAGAAAAAGATGCTTCTCTTATGATGATGATGATGATGATGATGATGATG 1346  
 Db 961 CATGTGAAGAAAAAGATGCTTCTCTTATGATGATGATGATGATGATGATGATGATG 1020  
 QY 1347 AAGTTGAGCTCGTGTGAGAGCTTACACATTAAGTTCGAGAAAGATGTCCTTATTCAC 1406  
 Db 1021 AAGTTGAGCTCGTGTGAGAGCTTACACATTAAGTTCGAGAAAGATGTCCTTATTCAC 1080

QY 1407 CCTGAATACGTTGCTCTATTTTGAACGAGCTGGCGAATGAAGATGCGGTGTTACTGTG 1466  
 Db 1081 CCTGAATACGTTGCTCTATTTTGAACGAGCTGGCGAATGAAGATGCGGTGTTACTGTG 1140  
 QY 1467 GATACCGCATGTGCATATGTGTGCAATGCGAGTACATTCGAATTCGAGAGGAAACGGGC 1526  
 Db 1141 GATACCGCATGTGCATATGTGTGCAATGCGAGTACATTCGAATTCGAGAGGAAACGGGC 1200  
 QY 1527 GACTTTGGGGTTCATTCGCGCAAGGAGTGGCTAATGCGTTCATGCGATTTGGT 1586  
 Db 1201 GACTTTGGGGTTCATTCGCGCAAGGAGTGGCTAATGCGTTCATGCGATTTGGT 1260  
 QY 1587 GCGCAAGTGTTCATTCGAACCGCGAGGTATTCGATGATGATGATGATGATGATGATG 1646  
 Db 1261 GCGCAAGTGTTCATTCGAACCGCGAGGTATTCGATGATGATGATGATGATGATGATG 1320  
 QY 1647 ATGCTGCTGGGTGAGCTTCTGACCGTTAAGTTCGACCACTTCCGCTGAAGGCTGTG 1706  
 Db 1321 ATGCTGCTGGGTGAGCTTCTGACCGTTAAGTTCGACCACTTCCGCTGAAGGCTGTG 1380  
 QY 1707 TTTAACAACAGTTCTTTGGGAGATGATGATGATGATGATGATGATGATGATGATGAT 1766  
 Db 1381 TTTAACAACAGTTCTTTGGGAGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
 QY 1767 TTGCTACTGACATGAGGAAGTGAATTCGACAGATTCGAGGCTGGCTGATATCAA 1826  
 Db 1441 TTGCTACTGACATGAGGAAGTGAATTCGACAGATTCGAGGCTGGCTGATATCAA 1500  
 QY 1827 TGGTACGATCACCGATTCGAGAAAGTTCGAGAGAGTCTAGCTGAGGCAATTCGAT 1886  
 Db 1501 TGGTACGATCACCGATTCGAGAAAGTTCGAGAGAGTCTAGCTGAGGCAATTCGAT 1560  
 QY 1887 CCGGACCTGTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1946  
 Db 1561 CCGGACCTGTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620  
 QY 1947 ATCACTGGGAAACAGTCAATGAGATTCAGCAAGGCGGCCAACCGTCTTGTGTA 2006  
 Db 1621 ATCACTGGGAAACAGTCAATGAGATTCAGCAAGGCGGCCAACCGTCTTGTGTA 1680  
 QY 2007 GAGTGAAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2063  
 Db 1681 GAGTGAAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1737

RESULT 11  
 US-10-781-014-89  
 : Sequence 89, Application US/10781014  
 : Publication No. US20040180408A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Pompeius, Markus  
 : APPLICANT: Kroeger, Burkhard  
 : APPLICANT: Schröder, Hartwig  
 : APPLICANT: Zeider, Oskar  
 : APPLICANT: Haberer, Gregor  
 : TITLE OR INVENTION: CORN/BERCTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
 : TITLE OR INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY  
 : FILE REFERENCE: BGI-126CPCN  
 : CURRENT APPLICATION NUMBER: US/10/781,014  
 : PRIOR FILING DATE: 2004-02-17  
 : PRIOR APPLICATION NUMBER: US 09/602,740  
 : PRIOR FILING DATE: 2000-06-23  
 : PRIOR APPLICATION NUMBER: 60/141,031  
 : PRIOR FILING DATE: 1999-06-25  
 : PRIOR APPLICATION NUMBER: 60/143,208  
 : PRIOR FILING DATE: 1999-07-09  
 : PRIOR APPLICATION NUMBER: 60/151,572  
 : PRIOR FILING DATE: 1999-08-31  
 : PRIOR APPLICATION NUMBER: DE 19931412.8  
 : PRIOR FILING DATE: 1999-07-08  
 : PRIOR APPLICATION NUMBER: DE 19931413.6  
 : PRIOR FILING DATE: 1999-07-08



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; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931424.1
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931428.4
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 784
; SEQ ID NO 89
; LENGTH: 944
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(921)
; OTHER INFORMATION: PRXA00635
US-10-781-014-89

```

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Query Match      43.7%; Score 944; DB 17; Length 944;
Best Local Similarity 100.0%; Pred. No. 4.9e-295;
Matches 944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1143 GGTACGGATTTCCCTTATTCGATTTCTTCTTAAAGCAACGTTGCCAGGTGATATC 1202
DB 1 GGTACGGATTTCCCTTATTCGATTTCTTCTTAAAGCAACGTTGCCAGGTGATATC 60
QY 1203 AACGGTCCGACATTTGTCGACGTCACGCGTGAAGTATCCGGTACCGGTGATTTGCT 1282
DB 61 AACGGTCCGACATTTGTCGACGTCACGCGTGAAGTATCCGGTACCGGTGATTTGCT 120
QY 1263 GCAACATATGAAAAATTTTGGCTCATGTGAAGAAAAAGATCTTCTCTTGAT 1322
DB 121 GCAACATATGAAAAATTTTGGCTCATGTGAAGAAAAAGATCTTCTCTTGAT 180
QY 1323 CGGATGCTCAAGGCGACAGAGGTAAAGTGAAGTCTGGGTGAAGACATACACATAC 1382
DB 181 CGGATGCTCAAGGCGACAGAGGTAAAGTGAAGTCTGGGTGAAGACATACACATAC 240
QY 1383 GTCCGAAGCATGTGCTTATTCACCTGTAATACCTGCTCTTATTTGAAGAGCTGGCG 1442
DB 241 GTCCGAAGCATGTGCTTATTCACCTGTAATACCTGCTCTTATTTGAAGAGCTGGCG 300
QY 1443 GATAAGGATGCGGTGTTACTGTGATTAACGGGCAATGTGCAATGTGCGACATGAC 1502
DB 301 GATAAGGATGCGGTGTTACTGTGATTAACGGGCAATGTGCAATGTGCGACATGAC 360
QY 1503 ATCGAAGATCGGAGGAGACCGGCACTTTGTGGTTCAATTCGCCACCGGCAATGAGCT 1562
DB 361 ATCGAAGATCGGAGGAGACCGGCACTTTGTGGTTCAATTCGCCACCGGCAATGAGCT 420
QY 1563 AATGCGTTCCTCATGTGATTTGTCGCAAAAGTGTGATGAAACCGGCAATGAGCTGCG 1622
DB 421 AATGCGTTCCTCATGTGATTTGTCGCAAAAGTGTGATGAAACCGGCAATGAGCTGCG 480
QY 1623 ATGTGTGGCATGTGTGTTGGCATGCTGCTGGTGAAGCTTCTGACCGTTAAGCTGCAC 1682
DB 481 ATGTGTGGCATGTGTGTTGGCATGCTGCTGGTGAAGCTTCTGACCGTTAAGCTGCAC 540
QY 1683 CAATCTCCGCTGAAGCTGTGTGTTAAACAAGTTCTTTGGGCAATGTTGAAGTTGAG 1742
DB 541 CAATCTCCGCTGAAGCTGTGTGTTAAACAAGTTCTTTGGGCAATGTTGAAGTTGAG 600
QY 1743 ATCTGTGGAGGAGACAGCCAAATTTGTAACGACATGAGAAAGTGAATTTGCGCAGAG 1802
DB 601 ATCTGTGGAGGAGACAGCCAAATTTGTAACGACATGAGAAAGTGAATTTGCGCAGAG 660
QY 1803 ATTGCGCGCGCTGCGGGTATCAAAATCGTACCATACCGATCCGAAAGAAATTCGCGAG 1862
DB 661 ATTGCGCGCGCTGCGGGTATCAAAATCGTACCATACCGATCCGAAAGAAATTCGCGAG 720
QY 1863 CAGCTAGCTGAGGCAATGGCATTCTCTGGAACCTGTATGATCATGATTCGACGAATCT 1922

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DB 721 CAGCTAGCTGAGGCAATGGCATTCTCTGGAACCTGTATGATCATGATTCGACGAATCT 780
QY 1923 AATGCGCTGTGATCCCAACCATGACGTGGAAACAGTCAATGATTCGACGAAGCG 1982
DB 781 AATGCGCTGTGATCCCAACCATGACGTGGAAACAGTCAATGATTCGACGAAGCG 840
QY 1983 GCCACCGGAACCGCTTTGGTGAAGAGTGAAGCATGATGATTCGACCGCTTGAAC 2042
DB 841 GCCACCGGAACCGCTTTGGTGAAGAGTGAAGCATGATGATTCGACCGCTTGAAC 900
QY 2043 ATTAAGAAATATCTTCACTCCATGATGATGATGATGATGATGATGATGATGATGAT 2086
DB 901 ATTAAGAAATATCTTCACTCCATGATGATGATGATGATGATGATGATGATGATGAT 944

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## RESULT 12

```

US-09-965-825-3
; Sequence 3, Application US/09965825
; Patent No. US2002015099A1
; GENERAL INFORMATION:
; APPLICANT: DUSCH, Nicole
; APPLICANT: THOMAS, Hermann
; APPLICANT: THIERBACH, Georg
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENIC ACID UK
; FILE REFERENCE: 21354US0X
; CURRENT APPLICATION NUMBER: US/09/965,825
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: DE 10048604.5
; PRIOR FILING DATE: 2000-09-30
; PRIOR APPLICATION NUMBER: DE 10117085.8
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-965-825-3

```

```

Query Match      40.5%; Score 875; DB 9; Length 875;
Best Local Similarity 100.0%; Pred. No. 1.2e-272;
Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 705 TGCAGATGCGATGATGTTGTTGACAGGTTGAACGATTTGATCAACGATTCAGTCC 764
DB 1 TGCAGATGCGATGATGTTGTTGACAGGTTGAACGATTTGATCAACGATTCAGTCC 60
QY 765 ACCATGCGGGTAAAGTGTGCGGTGATGATTCCTGATATTCCTTAAGAAAGC 824
DB 61 ACCATGCGGGTAAAGTGTGCGGTGATGATTCCTGATATTCCTTAAGAAAGC 120
QY 825 GCAGTACCGTATCTTATTCCTTCAATTCCTTCTGCACTCTGATGTTCCG 884
DB 121 GCAGTACCGTATCTTATTCCTTCAATTCCTTCTGCACTCTGATGTTCCG 180
QY 885 GATCTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 944
DB 181 GATCTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 945 TTTGCGGTGCGGCGTGAAGATGCTCCGCGCAGAGTTTGAAGTTGGCGGAGAAAT 1004
DB 241 TTTGCGGTGCGGCGTGAAGATGCTCCGCGCAGAGTTTGAAGTTGGCGGAGAAAT 300
QY 1005 AATTCACCATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1064
DB 301 AATTCACCATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 1065 GAGGTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1124
DB 361 GAGGTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420

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Oy	1125	GATCGCTGATTTCTTAATTTGGGTAAACGAAATTTCCCTTAATTTGAAATTTCTTCTTAAGAACAAC	1184
Db	421	GATCGCTGATTTCTTAATTTGGGTAAACGAAATTTCCCTTAATTTGAAATTTCTTCTTAAGAACAAC	480
Oy	1185	GTTGCCACAGTGGATATCAACGGTGGCGCAATTGGTGCACGTAACAGCGTAAGTATCG	1244
Db	481	GTTGCCACAGTGGATATCAACGGTGGCGCAATTGGTGCACGTAACAGCGTAAGTATCG	540
Oy	1245	GTAGCCGGTAGTNGTTCGTGCACAACATCGAATAATTTTGCCCTCACTGTAAGAGAAAAACA	1304
Db	541	GTAGCCGGTAGTNGTTCGTGCACAACATCGAATAATTTTGCCCTCACTGTAAGAGAAAAACA	600
Oy	1305	GATCGTTCCTTCTTGTATCGAGTGTCAAGGCAACGACGGTAAGTGAAGCTCGGTGTGA	1364
Db	601	GATCGTTCCTTCTTGTATCGAGTGTCTAAGGCAACGACGGTAAGTGAAGCTCGGTGTGA	660
Oy	1365	GAGACGTACACAATACGTGAGAGACATGTGCTTATTTCACTCGTAATACGTGGCTCT	1424
Db	661	GAGACGTACACAATACGTGAGAGACATGTGCTTATTTCACTCGTAATACGTGGCTCT	720
Oy	1425	AATTTGAACGAGCTGCGGATPAAGAGTGCGGTGTACTGTGGAATACCGGACATGNCAT	1484
Db	721	AATTTGAACGAGCTGCGGATPAAGAGTGCGGTGTACTGTGGAATACCGGACATGNCAT	780
Oy	1485	GTTGGCATGCGAGGTACATCGAGATCGAGAGAACGCGCGACTTTGTGGGTTCATTG	1544
Db	781	GTTGGCATGCGAGGTACATCGAGATCGAGAGAACGCGCGACTTTGTGGGTTCATTG	840
Oy	1545	CGCCACGGCACGATGCGTAAATGCGTTGCTCATGTC	1579
Db	841	CGCCACGGCACGATGCGTAAATGCGTTGCTCATGTC	875

```

RESULT 13
US-10-143-856-5
; Sequence 5, Application US/10143856
; Publication No. US20030109014A1
; GENERAL INFORMATION:
; APPLICANT: BURKE, KEVIN
; APPLICANT: DUNICAN, L. K.
; APPLICANT: MCCORMACK, ASHLING
; APPLICANT: STAPLETON, CLIONA
; APPLICANT: MOCKEL, BETTINA
; APPLICANT: THIERBAUGH, GEORG
; TITLE OF INVENTION: Process for the fermentative preparation of
; TITLE OF INVENTION: with amplification of the tkt gene
; FILE REFERENCE: MAS/021123/282432
; CURRENT APPLICATION NUMBER: US/10/143, 856
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/986, 649
; PRIOR FILING DATE: 17-03-2000
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-10-143-856-5

```

Query Match	40.5%	Score 875	DB 15	Length 875
Best Local Similarity	100.0%	Pred. No. 1.2e-272		
Matches 875; Conservative	0	Mismatches 0	Indels 0	Gaps 0

QY 705 TCGAGAGATGGTGAATGGTGGTGAAGCAGGGGTGAACGCAATTGGATCAACGGATTCACTGC 764

Dd 1 TCGCAGATGGTGAATGGTGGTGAAGCAGGGGTGAACGCAATTGGATCAACGGATTCACTGC 60

QY 765 ACCATGCGCGGGTAAAGGTGTGTGGTGTAGTGAATTCCTGGTATATCGCTAAGAGAAGAC 824

Dd 61 ACCATGCGCGGGTAAAGGTGTGTGGTGTAGTGAATTCCTGGTATATCGCTAAGAGAAGAC 120

QY 825 GCAGGTGACGTACTTATTCGAATTCGAATTTCTTTCGCACTCCTGTGGTGTCCG 884

Db	121	GCAGGTACGGTACTTATTCAAATTCACACTATTCTTCGGCACTCGTGGTGTCCG	180
Qy	885	GATCTTACTGAGGCTGCAAGCCCTGATGAGGCGATTAAACAAGCTAACTCTCACTTG	944
Db	181	GATCTTACTGAGGCTGCAAGCCCTGATGAGGCGATTAAACAAGCTAACTCTCACTTG	240
Qy	945	TTCTGCGGTGCGGGCGTGAAGAAAGTCTGCGCGCAGAGGATTGGAAGTGGCGGAGAAATT	1000
Db	241	TTCTGCGGTGCGGGCGTGAAGAAAGTCTGCGCGCAGAGGATTGGAAGTGGCGGAGAAATT	300
Qy	1005	AAATCACCGAATCGGGCATGCGCTGGGTGTGAACAGTACATCCACATGAGAAATCGTTT	1066
Db	301	AAATCACCGAATCGGGCATGCGCTGGGTGTGAACAGTACATCCACATGAGAAATCGTTT	360
Qy	1065	GAGGTCCGCAATGTCTGGCTCTGCTGTGTTACGGCGCTCGCTGGTGAATGCTCCATGAGCG	1122
Db	361	GAGGTCCGCAATGTCTGGCTCTGCTGTGTTACGGCGCTCGCTGGTGAATGCTCCATGAGCG	420
Qy	1125	GATCTGCGATTCTTATTTGGGTGAACGAAATTTCCCTTATTCGATTTCCCTCTTAAAGCAAC	1188
Db	421	GATCTGCGATTCTTATTTGGGTGAACGAAATTTCCCTTATTCGATTTCCCTCTTAAAGCAAC	480
Qy	1185	GTTGCCCAAGTGGATTAATCAACGCTGCGCAATTGGTTCAGACGTAACACGGTGAAGTATCG	1244
Db	481	GTTGCCCAAGTGGATTAATCAACGCTGCGCAATTGGTTCAGACGTAACACGGTGAAGTATCG	540
Qy	1245	GTTGACCCGGTGAATGTTGCTGCAACAATCGAAATAATTTTGCTCATGTGAAGGAAAAACA	1300
Db	541	GTTGACCCGGTGAATGTTGCTGCAACAATCGAAATAATTTTGCTCATGTGAAGGAAAAACA	600
Qy	1305	GATCGTTCTCTCTTGATTCGGATGCTCAAGGCAACGAGCGTAAATTGAAGCTCGGTGTA	1366
Db	601	GATCGTTCTCTCTTGATTCGGATGCTCAAGGCAACGAGCGTAAATTGAAGCTCGGTGTA	660
Qy	1365	GAGACGTACACATAACGTGAGAGAGGATGTGCTTATTCACCCCTGAATACGTTGCTCT	1422
Db	661	GAGACGTACACATAACGTGAGAGAGGATGTGCTTATTCACCCCTGAATACGTTGCTCT	720
Qy	1425	ATTTTGAACGAGCTGCGCGGATPAAGATGCGGTGTTTACTGTGATATCCGGCATGTGCAT	1488
Db	721	ATTTTGAACGAGCTGCGCGGATPAAGATGCGGTGTTTACTGTGATATCCGGCATGTGCAT	780
Qy	1485	GTTGGGCAATGCGAGGTATCATGAATTCGAGAGGAAACGCGGACTTTGTGGTTCATTTC	1544
Db	781	GTTGGGCAATGCGAGGTATCATGAATTCGAGAGGAAACGCGGACTTTGTGGTTCATTTC	840
Qy	1545	CGCCACGGCAACGATGGCTTAATGCGTTGCGCTATGC	1579
Db	841	CGCCACGGCAACGATGGCTTAATGCGTTGCGCTATGC	875

```

RESULT 14
US-10-078-167-6
; Sequence 6, Application US/10078167
; Publication No. US20030119154A1
; GENERAL INFORMATION:
; APPLICANT: Dunican, Rita
; APPLICANT: McCormack, Ashling
; APPLICANT: Stapleton, Cliona
; APPLICANT: Burke, Kevin
; APPLICANT: Mockel, Bettina
; TITLE OF INVENTION: Process for the preparation of L-amino acids using
; TITLE OF INVENTION: a gene encoding 6-Phosphogluconate Dehydrogenase
; FILE REFERENCE: 990229 BT-US-8
; CURRENT APPLICATION NUMBER: US/10/078,167
; CURRENT FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; US-10-078-167-6

```

Query Match	40.5%	Score 875;	DB 15;	Length 875;
Best Local Similarity	100.0%	Pred. No. 1.2e-272;		
Matches 875; Conservative	0;	Mismatches 0;	Indels 0.	Gaps 0

QY	705	TCGAGATGCGTAATGCGTGTGTGACACGAGGTGAACGATTTTGATCACCGCATTCAGTCC	764
Db	1	TGCGAGATGCGTAATGCGTGTGTGACACGAGGTGAACGATTTTGATCACCGCATTCAGTCC	60
QY	765	ACCATGCGCGGTAAAGGTGTGTGCGGTGTGTGATTTCTGTGGAATTCGCTTAAGAGAAC	824
Db	61	ACCATGCGCGGTAAAGGTGTGTGCGGTGTGTGATTTCTGTGGAATTCGCTTAAGAGAAC	120
QY	825	GCAGGTACCGGTACTTATTTCCAAATTCACATTTTCTTGTGCACTCTGTGGTGTCCG	884
Db	121	GCAGGTACCGGTACTTATTTCCAAATTCACATTTTCTTGTGCACTCTGTGGTGTCCG	180
QY	885	GATCCCTACTAGAGCTGCAGCGCTGTGTGGAAGGAGATTAAACAAGCTAAATGCTGTCACTTGG	944
Db	181	GATCCCTACTAGAGCTGCAGCGCTGTGTGGAAGGAGATTAAACAAGCTAAATGCTGTCACTTGG	240
QY	945	TTTCGCGGTGCGCGCGCTGGAAGAAATGCTCGCGCGAGGTGTGAGTTGGCGGAGAAAT	1004
Db	241	TTTCGCGGTGCGCGCGCTGGAAGAAATGCTCGCGCGAGGTGTGAGTTGGCGGAGAAAT	300
QY	1005	AAATCAACCATCGGGCATGCGCGTGGGTGTGAACGCTACATCCAGCATGAGAAATCCGTTT	1064
Db	301	AAATCAACCATCGGGCATGCGCGTGGGTGTGAACGCTACATCCAGCATGAGAAATCCGTTT	360
QY	1065	GAGGTGGCATGTCTTGACTGTGTGTGAACGCGCTGCGCGTGAATGCGTCAATGAGGG	1124
Db	361	GAGGTGGCATGTCTTGACTGTGTGTGAACGCGCTGCGCGTGAATGCGTCAATGAGGG	420
QY	1125	GATTCGCTGATTCATATTGAGTGAACGGAATTTCCCTATTTCTGATTTCTTCTTAAGAACAAC	1184
Db	421	GATTCGCTGATTCATATTGAGTGAACGGAATTTCCCTATTTCTGATTTCTTCTTAAGAACAAC	480
QY	1185	GTTGCCCAAGGTGATATCAACGGTGCAGCATTTGTGTGACGTACACGCGTGAAGTATCCG	1244
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QY	1245	GTTGACCGGTGATGTTGCTGCAACAATGGAATAATTTTGTGCTGATGTGAAGAAAAACA	1304
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QY	1305	GATGCTTCTTCTCTGTGATCGGATGCTCAAGGACACAGCGGTAAAGTGAAGCTCGGTGTA	1364
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QY	1365	GAGACGTACACATAACGTCGGAAGAGCATGTGCTTAATCAACTGAAATACGTTGCCCT	1424
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QY	1425	ATTTTGAACAGAGCTGTGGGATTAAGATGCGGTGTTATCTGTGGAATCCGGCATGTGCAAT	1484
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QY	1485	GTTGGGATGCGGAGTACATCGAATAATCCGAGGGAACGCGCATTTGTGTGTTCAATC	1544
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QY	1545	CGCCACGGCACGATGCTAATCGTGTGCTCAATG	1579
Db	841	CGCCACGGCACGATGCTAATCGTGTGCTCAATG	875

RESULT 15  
US-10-336-049-6

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sequence 6, Application US/10336045
Publication No. US20030175911A1
GENERAL INFORMATION:
APPLICANT: Hans, Stephan
APPLICANT: Bathe, Brigitte

```

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1  / APPLICANT: Reith, Alexander
2  / APPLICANT: Thierbach, Georg
3  / APPLICANT: Kreutzner, Caroline
4  / APPLICANT: Mockel, Bettina
5  / TITLE OF INVENTION: Process for the Preparation of L-Amino Acids with Amplification o
6  / TITLE OF INVENTION: the zwf Gene
7  / FILE REFERENCE: 7601/80158
8  / CURRENT APPLICATION NUMBER: US/10/336,049
9  / CURRENT FILING DATE: 2003-01-30
10 / NUMBER OF SEQ ID NOS: 37
11 / SOFTWARE: PatentIn version 3.1
12 / SEQ ID NO 6
13 /
14 / LENGTH: 875
15 /
16 / TYPE: DNA
17 /
18 / ORGANISM: Corynebacterium glutamicum
19 /
20 / US-10-336-049-6

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Query Match	40.5%;	Score 875;	DB 15;	Length 875;
Best Local Similarity	100.0%;	Pred. No. 1.2e-272;		
Matches 875; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

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OY	765	ACCATG	CGGGTAAAG	GTGTCGG	TGATG	ATGATTC	CTGTG	ATATG	CTTAAG	AGAC	824	
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OY	825	GCAAGTGA	CGGTACTT	ATATTC	CAATTC	ATATTC	CTTCTG	GCAC	TCCTG	TCGTCCG	884	
Db	121	GCAAGTGA	CGGTACTT	ATATTC	CAATTC	ATATTC	CTTCTG	GCAC	TCCTG	TCGTCCG	180	
OY	885	GATCCTA	CTAGG	CGTGCAG	CGCTGTG	TGATG	ATTAACA	CGCTA	AGTCTG	CATTTG	944	
Db	181	GATCCTA	CTAGG	CGTGCAG	CGCTGTG	TGATG	ATTAACA	CGCTA	AGTCTG	CATTTG	240	
OY	945	TTCTGCG	GTGCGGGGTGA	AGATTC	TCTG	CGCGG	CAGGTG	TGAG	TTGGCG	GAGAAAT	1004	
Db	241	TTCTGCG	GTGCGGGGTGA	AGATTC	TCTG	CGCGG	CAGGTG	TGAG	TTGGCG	GAGAAAT	300	
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Db	361	GAGGTG	GCATG	CTGCG	CTGCTTG	TGTGA	CGCGC	CTGCTG	TGATG	TCGCAATG	AGGCG	420
OY	1125	GATCTG	CTGATCTT	ATATGG	TGACGATTC	CTTATCTG	ATTTCTG	CTCTA	ATAG	CATC	1184	
Db	421	GATCTG	CTGATCTT	ATATGG	TGACGATTC	CTTATCTG	ATTTCTG	CTCTA	ATAG	CATC	480	
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Db	541	GTGACG	GTGATG	TGTCG	CAACAT	TCGAAAT	TTTCC	CTCATG	TGAAG	AAAAACA	600	
OY	1305	GATGTC	CTTCTT	CTTATG	TGATG	TCGACG	CAACG	AGCTGA	ATG	TGAGCTG	CGGTGTA	1364
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OY	1425	ATTTTGA	CGAG	CTGG	CGATAG	AGATCG	GTGTTA	CTG	TGAG	ATACCG	GAATG	1484
Db	721	ATTTTGA	CGAG	CTGG	CGATAG	AGATCG	GTGTTA	CTG	TGAG	ATACCG	GAATG	780

QY 1485 GTGTGGCATGCGAGGTACATCGAGATCCGAGGGAACCGCGACTTGTGGGTTCAATTC 1544  
Db 781 GTGTGGCATGCGAGGTACATCGAGATCCGAGGGAACCGCGACTTGTGGGTTCAATTC 840  
QY 1545 CGCCACGGCAGATGGCTAATGCCGTTGCTCATGC 1579  
Db 841 CGCCACGGCAGATGGCTAATGCCGTTGCTCATGC 875

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Job time : 1133.56 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: January 15, 2005, 08:20:57 ; Search time 140 Seconds  
(without alignments)  
2939.620 Million cell updates/sec

Title: US-09-965-825-2

Perfect score: 2985

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 824507 seqs, 355394441 residues

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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Issued Patents NA.\*  
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6: /cgm2\_6/ptodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1338	44.8	1746	4	US-09-543-681A-4139
2	1317.5	44.1	1719	4	US-10-096-571-1
3	1312.5	44.0	1749	4	US-09-489-039A-4884
4	1068.5	35.8	1737	4	US-09-252-991A-7335
5	990.5	33.2	1448	4	US-10-096-571-8
6	948.5	31.8	1293	4	US-09-489-039A-4905
7	927	31.1	1454	4	US-10-096-571-7
8	790.5	26.5	7900	4	US-08-965-171E-138
9	790.5	26.5	7900	4	US-08-781-586A-138
10	749.5	25.1	1761	3	US-09-134-001C-1619
11	744.5	24.9	2577	4	US-09-252-991A-8458
12	744.5	24.9	2754	4	US-09-252-991A-8530

C	13	693	23.2	1113	4	US-09-252-991A-7281	Sequence 7281, Ap
	14	686	23.0	1083	4	US-09-252-991A-7413	Sequence 7413, Ap
	15	643	21.5	1746	4	US-09-107-532A-3181	Sequence 3181, Ap
	16	586.5	19.6	1664976	4	US-08-916-421B-1	Sequence 1, Appl1
	17	586.5	19.6	1664976	4	US-09-692-570-1	Sequence 1, Appl1
	18	526	17.6	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
	19	521.5	17.5	1701	4	US-09-583-110-1223	Sequence 1223, Ap
	20	521.5	17.5	6211	4	US-08-961-527-8	Sequence 8, Appl1
	21	520	17.4	4403765	3	US-09-103-840A-2	Sequence 2, Appl1
	22	516.5	17.3	1947	4	US-09-489-039A-840	Sequence 367, Ap
	23	516	17.3	1689	4	US-09-489-039A-840	Sequence 840, Ap
	24	514	17.2	2111	4	US-10-096-571-11	Sequence 11, Appl1
	25	514	17.2	2111	4	US-10-096-571-13	Sequence 13, Appl1
	26	514	17.2	2841	3	US-08-452-075-1	Sequence 1, Appl1
	27	514	17.2	2841	3	US-09-231-061-1	Sequence 1, Appl1
	28	514	17.2	2841	3	US-09-011-762-5	Sequence 5, Appl1
	29	507	17.0	1776	4	US-09-583-110-152	Sequence 152, Ap
	30	507	17.0	25002	4	US-08-961-527-8	Sequence 48, Appl1
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	35	481	16.1	1689	4	US-09-543-681A-199	Sequence 199, Ap
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	37	466.5	15.6	3831	4	US-09-710-279-3959	Sequence 3959, Ap
	38	455	15.2	798	1	US-09-252-991A-7166	Sequence 7166, Ap
	39	449	15.0	1728	1	US-08-403-866-12	Sequence 12, Appl1
	40	449	15.0	2231	1	US-08-403-866-14	Sequence 14, Appl1
	41	449	15.0	12720	1	US-08-403-866-11	Sequence 11, Appl1
	42	448	15.0	1969	1	US-07-737-851-3	Sequence 3, Appl1
	43	447.5	15.0	1665	3	US-09-134-001C-1565	Sequence 1565, Ap
	44	447.5	15.0	1665	4	US-09-710-279-1413	Sequence 1413, Ap
	45	447.5	15.0	4093	4	US-09-710-279-3793	Sequence 3793, Ap

#### ALIGNMENTS

RESULT 1  
US-09-543-681A-4139  
Sequence 4139, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.1002-001  
CURRENT APPLICATION NUMBER: US/09/543,681A  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128,706  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 4139  
LENGTH: 1746  
TYPE: DNA  
ORGANISM: Proteus mirabilis  
US-09-543-681A-4139

#### Alignment Scores:

Pred. No.: 4.54e-139 Length: 1746  
Score: 1338.00 Matches: 272  
Percent Similarity: 65.55% Conservative: 101  
Best local Similarity: 47.80% Mismatches: 190  
Query Match: 44.82% Indels: 6  
DB: Gaps: 6

US-09-965-825-2 (1-579) x US-09-543-681A-4139 (1-1746)

Cy 6 AAlGdInleuileAspThrleuGAlGlyVallysaRgIlyrGlyleuVal 25  
Db 40 GCAACCTATATTCCTAAAGTCTCCATATGCAAGGTGTGAAGCATTTTGGGGGTACG 99  
Cy 26 GYAAspserleuAspProIleValAlaPAlaValAlaRgIn---SerApIleGluTrpVal 44





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QY 1 MetAlaHisertyValagluInleuThreugluValagluValylarg 20
Db 1 ATGAAACAAAGCGTTCATATCGCCAAACACCTGATCGGCGGGGTAAGCGC 60
QY 21 IleTyrglyLeuValGlyAspSerLeuAsnProIleValAspAlaVal--ArgGlnSer 39
Db 61 ATCTGGGAGTCAACAGCGACTCTGAAACGCTCTTGATGACATCTTAATGCAATGGGC 120
QY 40 AspIleGluTrpValHisValArgAsnGluValAlaAlaPheAlaAlaGluVal 59
Db 121 ACCATTCAGTGGATGTCACCCGCCACAGAAAGTGGCGGCTTTCGCGCTGGCGCTGAA 180
QY 60 SerLeuIleThrglyGluLeuAlaValCysAlaAlaSerCysGlyProGlyAsnThrHis 79
Db 181 GCAACAATTAGCGGAAGACTGGCGGTCTGCGCGGATGTCGGCGCCCGGCAACTGCAC 240
QY 80 LeuIleGluGlyLeuTyrrAspSerHisArgAsnGlyAlaValValLeuAlaIleAsn 99
Db 241 TTAAATCAACGGCTGTTGATGTCACCGCAATCACTTCGCGTACCTGGCAATGGCGCT 300
QY 100 HisIleProSerAlaGluIleGlySerThrPheGluGluThrHisProGluIleLeu 119
Db 301 CATATTCCTTCACGAAATTTGGAGCGCTATTTCCAGAAACCCACCAAGAGCTA 360
QY 120 PheIleGluCysSerGlyTyrrCysGluMetValAsnGlyGlyGluGlyValArgIle 139
Db 361 TTCCGCGAATGTAATCACTATGTCAGAGTGTTCACGCGCGAGCAGATCCCAAGTA 420
QY 140 LeuHisAlaAlaIleGlnSerThreAlaGlyGlyValSerValValIlePro 159
Db 421 CTGCGCATTCGCAAGCGCAAGCGGCTTAAACGTCGTCGCTTCGCTTCATCA 480
QY 160 GlyAspIleAlaValGluAspAlaGlyAspGlyThrTyrrSerAsnSerThrIleSer 179
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QY 180 GlyThrProValValPheProAspProThrgluAlaAlaAlaLeuValGluAlaIleAsn 199
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QY 200 AsnAlaIleSerValThrLeuPheCysGlyValGlyValValAsnAlaArgAlaGluVal 219
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QY 220 LeuGluLeuAlaGlyValIleValSerProIleGlyHisAlaAlaGlyGlyGluTyrr 239
Db 658 GTTAGATTTCGCGGAAATTTAAAGCGCTATTTGTCATGCTTCGCGGTAAGAACAT 717
QY 240 IleGlnHisGluAsnProPheGluValGlyMetSerGlyLeuLeuGlyTyrrGlyValCys 259
Db 718 GTCAATATACATATTCGTATGATGTTGATGACCGGTTATCGGCTTCGTCAAGT 777
QY 260 ValAspAlaSerAsnGluValAspLeuLeuIleLeuLeuGlyThrAspPheProTyrrSer 279
Db 778 TTCATATACATGATGAAAGCGGACAGCTAGTGTACCTGCGCACGCAATTCCTTACGCG 837
QY 280 AspPheLeuProIleAsp--AsnValAlaGluValAspIleAsnGlyAlaHisIleGly 298
Db 838 GCCCTTCAACCGGACGATGCGAAATCATTCAGATGTAATCAACCGGACGATCGCGC 897
QY 299 ArgArgThrThrValTyrrProValThrGlyAspValAlaAlaThrIleGluAsnIle 318
Db 898 GCTCAACGACAGTGGATATGCACTGTCGCGCAATTCAGATGATCTTCGTCGCAATG 957
QY 319 LeuProHisValIleGlyValThrAspArgSerPheLeuAspArgMetLeuValAlaHis 338
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QY 399 ThrArgAspPheValGlySerPheArgHisGlyThreAlaAlaAsnAlaLeuProHisAla 418
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QY 419 IleGlyAlaGlnSerValAspArgAsnArgGluValIleAlaMetCysGlyAspGlyGly 438
Db 1246 CTGGGTGCGGAGGAGCAAGAGCCAGAACTGACAGTGTCTCCATGTGCGCGGATGGCGGT 1305
QY 439 LeuGlyMetLeuGlyGluLeuLeuThrValIleLeuHisIleGlnLeuProLeuValAla 458
Db 1306 TTAGCAATGTTGAGGCGAATTCCTCTCACTAGTGCAGATGAAACTGCAAGTGAATAATT 1365
QY 459 ValValPheAsnAsnSerSerLeuGlyMetValIleValLeuGluMetLeuValGluGlyGln 478
Db 1366 GTGCTCTTTAAACAACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1425
QY 479 ProGluPheGlyThrAspHisGluGluValAsnPheAlaGluIleAlaAlaAlaGly 498
Db 1426 TTGACTGACGCAACCGAATCAACAGCAACAACCTTCCGCGATTCGCGAAGCGTGGCGC 1485
QY 499 IleIleSerValArgIleThrAspProIleValArgGluGluLeuAlaGluAlaLeu 518
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QY 519 AlaTyrrProGlyProValLeuIleAspIleValThrAspProAsnAlaLeuSerIlePro 538
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QY 559 GlyGlyValGlyAlaMetIleAspLeuAlaArgSerAsn 572
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RESULT 3
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; Sequence 4884, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 4884
; LENGTH: 1749
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-4884

Alignment Scores:
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Score: 1312.50 Matches: 266
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Best Local Similarity: 46.34% Mismatches: 196
Query Match: 43.97% Indels: 7
DB: 4 Gaps: 6

US-09-965-825-2 (1-579) x US-09-489-039A-4884 (1-1749)

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QY 40 AspIleGlnTyrValHisValArgAsnGlnGlnAlaAlaAlaAlaAlaAlaGlyValGlu 59
Db 151 ACCATGACATGATGCCACCCCGACAGAAAGAGTGGCGCTTCCGCGCTGGCGCGGAA 210
QY 60 SerLeuIleThrGlyLeuLeuAlaValCysAlaAlaSerCysGlyProGlyAsnThrHis 79
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QY 120 PheLeuGlnCysSerGlyTyrCysGluMetValAsnGlyGlyGlnGlyValArgIle 139
Db 391 TTCGGAGATGACCATTAATCTGCGAACTGTCTCACGGCGGACATCCCGAGGTG 450
QY 140 LeuHisHisAlaIleGlnSerThrMetAlaGlyValGlyValSerValValIlePro 159
Db 451 CTGGCAGTGGCGATGCGTAAAGGCAATTAACCGCGCGTCTCGGTGTGTGGTCC 510
QY 160 GlyAspIleAlaIleGlnSerThrMetAlaGlyValGlyValSerValValIlePro 179
Db 511 GCGGATGTGGCCCTGAAGCCGCCCGGAAAGCC--ACACGCACTGTGTATCAGCG 567
QY 180 GlyThrProValValPheProAspProThrGlnAlaAlaAlaValGlnAlaIleAsn 199
Db 568 CCGCTGCCGACGATACCCCGCGGAGAAAGCTGCGCAAGCTGGCGAGCTTAATTCGC 627
QY 200 AsnAlaIleSerValThrLeuPheCysGlyValAlaGlyValIleValAsnAlaArgAlaGlnVal 219
Db 628 TACTCAGACATATGCGGCTCATGTGGCGAGCGGTGCCCGCGCCACACAGAACTG 667
QY 220 LeuGluLeuAlaGluValIleLeuSerProIleGlyHisAlaLeuGlyValIleGlyVal 239
Db 668 GTGAGTTCGACGCCAAATTAAGCCCATCTCCACGCGCTGCGCAAGAC 747
QY 240 IleGlnHisGluAsnProPheGlnValAlaGlyMetSerGlyLeuLeuGlyTyrGlyAlaCys 259
Db 748 GTGAGTACGACAAACCGGTACGATGTGGCATGACCGGCTGATGTGCTTCTCTGCG 807
QY 260 ValAspAlaSerAsnGlnAlaAspLeuLeuLeuGlnGlyThrAspPheProTyrSer 279
Db 808 TTCACACATGATGAACGCGGATACCTGATCTGTGGGACCCAGTTCCCTATCCG 867
QY 280 AspPheLeuProTyrAsp--AsnValAlaGlnValAspIleAsnGlyAlaHisIleGly 298
Db 868 GCGTTTCAACCGACCGGAAATTAATTCAGATGACATCAACCCCGGACATCGGC 927
QY 299 ArgArgThrValIleValTyrProValThrGlyAspValAlaAlaIleGlnLeuIle 318
Db 928 GCACACAGTAAAGTGCATGGCGCTGTGGGCGATTAATTCAGCGCTGAAGGCGCTG 987
QY 319 LeuProHisValIleGlyValThrAspArgSerPheLeuAspArgMetLeuValHis 338
Db 988 CTGCGCTGTCTGAAAGAAACCGATTCGCACTCTCGATGAGCGCTGAG--CAC 1044
QY 339 GluArgIleLeuSerSerValAlaGluThrTyrThrHisAsnValGluValIleValPro 358
Db 1045 TATTCGGACCGCGGAAAGGCTCGACGATCTGGCTAAACCGACGATAA-----GCC 1098
QY 359 IleHisProGluTyrValAlaSerIleLeuAsnGluLeuAlaAspIleValAlaPhe 378

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Db 1099 ATTCACCCGCAATATCTGGCGGACAGCATGATCTTTTCCGATGAAGTCCATTTTC 1158
QY 379 ThrValAspThrArgMetCysAsnValThrHisAlaArgTyrIleGluAsnProGluGly 398
Db 1159 ACTGTATGTGGGACACCCGACCGTGTGGCGGACAGCTATGTCAA--ATGAATGCT 1215
QY 399 ThrArgAspPheValGlySerPheArgHisGlyThrMetAlaAsnAlaLeuProHisAla 418
Db 1216 AAAGCGCGCTGCTGGCTGTGTTTACACAGCTGATGCCAACCCCATGCGCAGGCC 1275
QY 419 IleGlyValAlaGlnSerValAspArgAsnArgGlnValIleAlaMetCysGlyAspArgIle 438
Db 1276 ATCGGCGCAAGGCACTGCGCGGACGAGCGGAGTGTAGTGGCATGTGGCGCGCGGG 1335
QY 439 LeuGlyMetLeuLeuGlnGlyLeuLeuValThrValIleValLeuHisGlnLeuProLeuValAla 458
Db 1336 TTCAAGCATGCTGATGGGCAATTTTCTGTGCTGGCGCAGATGAAGCTGCCGGTGAAGATT 1395
QY 459 ValValPheAsnAsnSerSerLeuGlyMetValIleValLeuGluMetLeuValGluGln 478
Db 1396 GTCATCTTTAAACAAGCGCTGGCTGTGGCGATGGAATGAAGCCGGGGCTAT 1455
QY 479 ProGluPheGlyThrAspHisGluGlnValAsnPheAlaGluIleAlaAlaAlaGly 498
Db 1456 CTCACCGACGATGCGGAGTCTCCAGATACCACTTGCGCGCATGCTGAGGCTCGCGT 1515
QY 499 IleLeuSerValArgIleThrAspProTyrValArgGlnGlnLeuAlaGlnAlaLeu 518
Db 1516 ATCAAGATGATACGGTTGAATAAACCTCCAGAGTGAATGAAGCGCTCAAGCGCTTC 1575
QY 519 AlaTyrProGlyProValLeuIleAspIleValThrAspProAsnAlaLeuSerIlePro 538
Db 1576 CCGACGACGATGCGGTGTGTGTGTCACGTCGTGCGCAAGAGAACTGGCATCCG 1635
QY 539 ProThrIleThrTyrGlnGlnValMetGlyPheSerIleValAlaThrArgThrValPhe 558
Db 1636 CCGCAGATACACTGACGACGACGCAAGGCTTTTACCTGTATATGTCTGGCGCATCATC 1695
QY 559 GlyGlyGlyValAlaGlyAlaMetIleAspLeuAlaArgSerAsn 572
Db 1696 ACGGCGCGCGGATGAGTATGATGAACTGCGGAACCAAC 1737

RESULT 4
US-09-252-991A-7335
/ Sequence 7335: Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ FILE REFERENCE: 107136.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ PRIOR FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 7335
/ LENGTH: 1737
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7335

Alignment Scores:
Pred. No.: 5.37e-109
Score: 1068.50
Percent Similarity: 61.15%
Best Local Similarity: 40.47%
Query Match: 35.80%
DB: 4
Length: 1737
Matches: 225
Conservative: 115
Mismatch: 207
Indels: 10
Gaps: 5

```



OTHER INFORMATION: 3' region of the delta poxb allele  
 NAME/KEY: misc feature  
 LOCATION: (1446) ..(1448)  
 OTHER INFORMATION: Stop codon of the delta poxb allele  
 US-10-096-571-8

## Alignment Scores:

Pred. No.:	2,02e-100	Length:	1448
Score:	990.50	Matches:	228
Percent Similarity:	54.45%	Conservative:	84
Best Local Similarity:	39.79%	Mismatches:	166
Query Match:	33.18%	Indels:	96
DB:	4	Gaps:	10

US-09-965-825-2 (1-579) x US-10-096-571-8 (1-1448)

```

QY 1 MetAlHisSerTyraIagluInleuIleAspThrLeuGluAlaGlnGlyValIysArg 20
Db 1 ATGAAACAAACGGTTGCACTTATATCGCAAAACCTGAAATCGGAGGGGTGAAACGC 60
QY 21 IleTyGlyLeuValGlyAspSerLeuAsnProIleValAspAlaVal---ArgGlnSer 39
Db 61 ATCTGGGAGTCAACAGCGCACTCTGAAACGGCTTACGTACAGCTTATATCGCATGAGC 120
QY 40 AspIleGluTrpValHisValArgAsnGluGluAlaAlaIlePheAlaIleGlyValGlu 59
Db 121 ACCATGAGTGGATGTCACCGCCCAAGAGAGTGGCGCTTGGCCGCTGGCGCTGAA 180
QY 60 SerLeuIleThrGlyGluLeuValAlaCysAlaIleAspCysGlyProGlyAsnThrHis 79
Db 181 GCACAACTAGCGGAGAACTGGCGGTCTGCGCGATGCTGGCGCGCAACCTTGAC 240
QY 80 LeuIleGlnGlyLeuTyraAspSerHisArgAsnGlyAlaIleValIleAlaSer 99
Db 241 TTAATCAACGCGCTTTCATTCATTCACCGCAATACGTTCCGATCGGATTCGCGCT 300
QY 100 HisIleProSerAlaGlnIleGlySerThrPhePheGlnGluThrHisProGlnIleLeu 119
Db 301 CATATTCCTCCAGCAAAATTCGACGGCGCTATTCACGAAACCCCAACCAAGACTA 360
QY 120 PheIysGluCysSerGlyTyraCysGluMetValAsnGlyGlyGlnGlnGlyValArgIle 139
Db 361 TTCGCCGATGATGACATATTCGAGCGGTTCACCGCGGAGCGAGATCCCAAGTA 420
QY 140 LeuHisIleAlaIleGlnSerThrMetAlaGlySerValIleValIlePro 159
Db 421 CTGGGATTCGCAATGCGCAAGCGGTGCTTAACCGTGGCGCTTCGTTGCTGTTTACCA 480
QY 160 GlyAspIleAlaIleGluAspAlaGlyAspGlyThrTyraSerAsnSerThrIleSerSer 179
Db 481 GCGCAGCGTGGCTTAAACCTGCGCCAGAGGGGCA---ACCATGCACCTGATTCATGCG 537
QY 180 GlyThrProValIlePheProAspProThrGluAlaAlaIleValIleLeuAsn 199
Db 538 CCAACACCAAGTGGAGCGCGGAGAAAGAAAGATTAACGCAACCTG----- 582
QY 200 AsnAlaIysSerValThrLeuPheCysGlyAlaGlyValIleValAsnAlaArgAlaGlnVal 219
Db 583 -----GCGCAACTG 591
QY 220 LeuGluLeuAlaGluIleIleIysSerProIleGlyHisAlaLeuGlyIleIysGlnTyra 239
Db 592 CTG-----CGTTAT 600
QY 240 IleGlnHisGluAsnProPheGluValGlyMetSerGlyLeuLeuGlyTyraIleAlaCys 259
Db 601 TCCAGCGCTTAAGGCGCAATTCAG----- 624
QY 260 ValAspAlaSerAsnGluAlaAspLeuLeuIleLeuLeuGlyThrAspPheProTyraSer 279
Db 624 ----- 624
QY 280 AspPheLeuProIleYsaAspAsnValAlaGlnValAspIleAsnGlyAlaHisIleGlyArg 299

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Db 625 -----CACTGGCGGC 636
QY 300 ArgThrThrValIysTyraProValThrGlyAspValAlaAlaThrIleGluAsnIleLeu 319
Db 637 CGTTA-CTAGTGAT---CCGAGATTCGCAAAATTC---GCCCTTCGCGTGCATGCTT 689
QY 320 ProHisValIysGluTyraThrAspArgSerPheLeuAspArgMetLeuIysAlaHisGlu 339
Db 690 CCATTGGTGAAGAAGAAAGCCGATCGCAAGTTCTGGATTAACGCGTGAAGATTAC--- 746
QY 340 ArgIleLeuSerSerValIleGluThrTyraThrHisAsnValGlyIleHisValProIle 359
Db 747 GCGACGCCCGCAAAAGGCGTGAACGATTGACTAAACGAGCGAGAA-----GCCAT 800
QY 360 HisProGluTyraValAlaSerIleLeuAsnGluLeuAlaAspIleAspAlaValPheThr 379
Db 801 CACCGCAATATCTGGCGGAGCAAAATTGATTCATTTGCCCGGATGACGCTATTTTCAC 860
QY 380 ValAspThrGlyMetCysAsnValIlePheAlaArgTyraIleGluAsnProGluGlyThr 399
Db 861 TGTGACGTTGGTACGCCAACGGTGGCGGACGCTTATCTAA---ATGAACGCAAG 917
QY 400 ArgAspPheValGlySerPheArgHisGlyThrMetAlaAsnAlaLeuProHisAlaIle 419
Db 918 CGTCGCTGTAGGTTGCTTAAACAGGTTGATGAGCTTAACGCGCATATCGGAGCGCTG 977
QY 420 GlyAlaGlnSerValAspArgAsnArgGlnValIleAlaMetCysGlyAspGlyValLeu 439
Db 978 GGTGGCCAGGCGCACAGAGCCAGAACAGTCAAGTGGTGGCATGTGGCGGATGGCGTTT 1037
QY 440 GlyMetLeuLeuGlyGluLeuLeuThrValIleIysLeuHisGlnLeuProLeuIleAlaVal 459
Db 1038 AGCATTTTATGAGGCGATTTCTCTCAGATGACGATGAACCTGCCGTAATAATTGTC 1097
QY 460 ValIleAsnAsnSerSerLeuGlyMetValIleIysLeuGluMetLeuValGlnGlyPro 479
Db 1098 GTCTTAAACACAGCGGTGCGCTTGTGGCGATGAGTGAAGAAAGCTGGTGGCTATTG 1157
QY 480 GluPheGlyThrAspHisGluGluValAsnPheAlaGluIleAlaAlaIleAlaGlyIle 499
Db 1158 ACTGACGCGACCGAACAACAAGCAAACTTCCCGCATTTGCCAAGCGTGGCGATT 1217
QY 500 IysSerValArgIleThrAspProIleValArgGlnGluLeuAlaGluAlaLeuAla 519
Db 1218 ACCGGTATCCGTTAGAAAGAAAGCGTCTGAAGTGAAGAGCCGCAACGCGCTTCTCC 1277
QY 520 TyrProGlyProValLeuIleAspIleValIleAspProAsnAlaLeuSerIleProPro 539
Db 1278 ATCGACGCGTCCGTTGGTGGTGAATGAGTGGTGGCCAAAGAGATTAAGCATTCACCG 1337
QY 540 ThrIleThrTrpGluGlnValMetGlyPheSerIleAlaAlaThrArgThrValPheGly 559
Db 1338 CAGATCAACTCGAACAAGCGCAAAAGTTTCAAGCTGTATATGCTGCGCGCAATCAACAC 1397
QY 560 GlyIleValGlyAlaMetIleAspLeuAlaArgSerAsn 572
Db 1398 GAGCGCGGTATGAAGTATGAACTGCGCAAAACAAAC 1436

```

## RESULT 6

US-09-489-039A-4905/C  
 Sequence 4905, Application US/09489039A  
 Patent No. 6610836  
 GENERAL INFORMATION:  
 APPLICANT: Gary Breton et al  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KUEBIELLA  
 FILE REFERENCE: 2709.2004001  
 CURRENT APPLICATION NUMBER: US/09/489,039A  
 PRIOR FILING DATE: 2000-01-27  
 PRIOR APPLICATION NUMBER: US 60/117,747  
 NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 4905  
 LENGTH: 1293  
 TYPE: DNA  
 ORGANISM: Klebsiella pneumoniae  
 US-09-489-039A-4905

## Alignment Scores:

Score:	8.13e-96	Length:	1293
Percent Similarity:	948.50	Matches:	191
Best Local Similarity:	65.69%	Conservative:	79
Query Match:	46.47%	Mismatches:	134
	31.78%	Indels:	7
	4	Gaps:	6

US-09-965-825-2 (1-579) x US-09-489-039A-4905 (1-1293)

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Qy 1 MetLahSserTYrAlaGluGluLeuLleAerPThrLeuGluAlaGlnGlyValIyAArg 20
Db 1218 ATGAACAAGACCGTGGCGCATACATTCGCAAAAGCTGGAACAGCCGGCGTGAACGT 1159
Qy 21 ILeTyrGluValAlaGlyAspSerLeuAerProIleValAaPheAlaVal---ArgGlnSer 39
Db 1158 ATCTGGGCGCTCACCGGAGATTCCTCATAGGATTAAGCGATAGCCTTAACCGCATGGCC 1099
Qy 40 AepIleGluTrpValHisValArgAangluGluAlaAlaAaPheAlaAlaGlyValAglu 59
Db 1098 ACCATCGACTGGATGCCACCGCGGACAGAGAGTGGCGGCTTGGCGGCGGCGGAA 1039
Qy 60 SerLeuIleThrGlyGluLeuAlaValAlaGlyAlaAaSerCyGlyTrpGlyValAerThrHis 79
Db 1038 GCGGACGCTGACCGCGGACGCTGGCGGCTGCGCGGCTGCGGACCGCGGACGCTGCAC 979
Qy 80 LeuIleGlnGlyLeuTyrAspSerHisAArgAangluAlaValIleValIleAaSer 99
Db 978 CTGATTAACGGTTGTGTGACTGTATGACCAACATGTCGCGGTCTGGCATGCGCGCC 919
Qy 100 HisIleProSerAlaGlnIleGlySerThrPhePheGlnGluTrpHisProGluIleLeu 119
Db 918 CACATCCCATCAGAGAAATGGGACGCGGCTATTTTCAGAAACCACTCCACAGAGCTG 859
Qy 120 PheIyGluCySerGlyTyrCyGluMetValAangluGlyGluGlnGlyValAglu 139
Db 858 TTCGCGGAGTCAACCATTAAGTGTCTCAAGCGGACAGCATGCCGAGGAGTG 799
Qy 140 LeuHisHisAlaIleGlnSerThrMetAlaGlyValIleValIleValIlePro 159
Db 798 CTGGACGCTGAGTGGCTGAAGGACGATGATTAACCGCGGCTGCTGGTGGTGTGTGCC 739
Qy 160 GlyAerIleAlaValyGluAaPheAlaGlyAaPheGlyTrpSerAaerThrIleSerSer 179
Db 738 GGCATGTGGCGCTGAAGCGCGCGCGGAAAGCGCC---ACGACGCACTGGATCATGCG 682
Qy 180 GlyThrProValValPheProAerProThrGluAlaAlaAlaValIleAaPhe 199
Db 681 CCGGTCGCGGACGCTCACCGCGGGAAGAAGAGCTGCGCAAGCTGGCGGACGATATGCG 622
Qy 200 AaAlaIyAaSerValThrLeuPheCyGlyValAgluValIyAaAlaAlaValIle 219
Db 621 TACTCCAGCAATATCGCGCTCATGTGCGGCGGCTTGGCGGCGCGGCGGCGGCGGCGGCGG 562
Qy 220 LeuGluLeuAlaGluValIleYSerProIleGluHisAlaAlaGluGlyValyGlnIly 239
Db 561 GTGAGTTCGCGACCGCAAAATTAAGCGCGCGCATCTGCCACGCGCTGCGGCGGAAAGAGAC 502
Qy 240 ILeGlnHisGluAaerProPheGluValAlaGlyMetSerGlyLeuGluGlyTyrGlyAla 259
Db 501 GTGAGTTCGCGACCGCGGATGATGTGGGAGTGAAGCGGCGGCTGATGCTTCTTCTGCGC 442
Qy 260 ValAaPheAaSerAangluAlaAaPheLeuLeuIleLeuGluGlyTrpAerProGlySer 279
Db 441 TTCCACACCATGATGAACCGGATGACCTGATCTGCTGGCGGCGGCGGCGGCGGCGGCGG 382
Qy 280 AaPheLeuProGlyAaPhe---AaValAlaGluValAaPheAaGluAlaHisGly 298
  
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Db 381 GCCTTACACCAACCGACGCGGAAATTAATCCAGATTCACATCAACCCCGGACGATCGGC 322
Qy 299 ArgAaGhrThrValIyGlyTrpProValThrGlyAaPheAlaAlaAaThrIleGluAaHis 318
Db 321 GCACACAGTAGTGAAGCATGCGCGTGGCGGATTAATGAAGCGGCGGCGGCGGCGGCGGCGG 262
Qy 319 LeuProHisValIyGluValyThrAaPheSerPheLeuAaPheAaGlyMetLeuValAaHis 338
Db 261 CTGCGCTGCTGCGAAGAGAAACCGATCGCATCTTCGATTAAGCGCGCTGAG---CAC 205
Qy 339 GluAaGlyLeuSerSerValAlaGluThrTyrThrHisAaValIleGlyValIlePro 358
Db 204 TATCGGACGCGCGGCAAAAGGCGTGCAGATGCTGCTGAACCGGATGA---GCC 151
Qy 359 ILeHisProGluTyrValAlaAaSerIleLeuAaGluLeuAlaAaPheAaPheAlaValAaPhe 378
Db 150 ATTACCGCGCAATATCTGGCGGACAGATGATGATTTGGCGGATGAAGATGCCATTTTC 91
Qy 379 ThrValAaPheThrGlyMetCyAaAaValTrpHisAlaAaGlyTrpIleGluAaPheGluGly 398
Db 90 ACTGTGATGTGCGGACCGGACCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 34
Qy 399 ThrAaAaPheValAlaGlySerPheAaGhrHisGly 409
Db 33 AAACCGCGCTGCTGGGCTGTTCAACCAAGCGC 1

RESULT 7
US-10-096-571-7
; Sequence 7, Application US/10096571
; Patent No. 6623944
; GENERAL INFORMATION:
; APPLICANT: RIBBING, MECHTHILD
; TITLE OF INVENTION: Process for the preparation of D-pantothenic acid and/or salts the
; FILE REFERENCE: 211499
; CURRENT APPLICATION NUMBER: US/10/096, 571
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: DE 10112102.4
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)_(1454)
; OTHER INFORMATION: Multigene DNA
; NAME/KEY: misc feature
; LOCATION: (1)_(56)
; OTHER INFORMATION: Technical-grade DNA/Residues of polylinker sequence
; NAME/KEY: misc feature
; LOCATION: (57)_(577)
; OTHER INFORMATION: Part of the 5' region (prox1) of the pox1 gene
; NAME/KEY: misc feature
; LOCATION: (578)_(646)
; OTHER INFORMATION: Technical-grade DNA/Residues of polylinker sequence
; NAME/KEY: misc feature
; LOCATION: (647)_(1398)
; OTHER INFORMATION: Part of the 3' region (prox2) of the pox2 gene
; NAME/KEY: misc feature
; LOCATION: (1399)_(1454)
; OTHER INFORMATION: Technical-grade DNA/Residues of polylinker sequence
US-10-096-571-7

Alignment Scores:
Pred. No.: 2.48e-93 Length: 1454
Score: 927.00 Matches: 216
Percent Similarity: 53.28% Conservative: 76
Best Local Similarity: 39.42% Mismatches: 156
  
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Db      2182 CCGTGCAGTGAATTAAATGGTGTAGTGGCGAACAATGCAGAAAGATGAGCTAACGGTAATTAATT 2241
Qy      224  GILUYAIELYSESPROILEGYNIALEALEUGLYGLYSGNLYRILEGNIHLEGLU 243
Db      2242 GAAATGGCTAAATATTCCTGTCAATTCATTCATCCAGCTAAACAATCTCCGAGAT 2301
Qy      244  AAnPProPhegluValGLYmetSerGLYleuSeuGLYtrGLYlaCYuValAspAlaser 263
Db      2302 CATCATATATAGTATCGGTAACCTTAGGTAAATCGGTACCAAAACATCTTATCAACATG 2361
Qy      264  AAnGLuAlaAspLeuLeuILEuLeuGLYThzAspPheProTYrSerAspPheLeuPro 283
Db      2362 CAGGAAGCGGATTTATTAATTATGTTGGTGTGTAACAACATATCATATGAGGATTACTTACCT 2421
Qy      284  LysAspAsnVal-----AlaGLInValAspLLeaNGLYlaNIaHILEGLYlaGATGTh 301
Db      2422 AAGAAATATATATAAGCATTCCAATTCAGCAAAATCTTAATAATTCGACATCGTTTC 2481
Qy      302  ThrVallyStryProValThzGLYAspValAlaAlaThzrILEGLuAsnILEuProHIs 321
Db      2482 AATTTAAATGTAGAAATTTGTTGGAGATGTAAATTCGGTTGCATCAGTTAACTGAAT 2541
Qy      322  VallySGILYstrAspAspSerPheLeuAspArgMetLeuValaNIaGLUaGLYs 341
Db      2542 ATTAAACATGTGTGCTGAAGACCACTTTTAACAACAACGTTA-----GAACGTAA 2592
Qy      342  Leu-----SerSerValValGLUThrThzrHIsaAnValGLYVNIHValProILE 359
Db      2593 GCGGTTTGGAGTAATAGGATGAGAACAGATTAATTAATTAATTAATTAATTAATTAATTA 2646
Qy      360  HIsProGLUTrYrValAlaSerILEuAsnGLUleuAlaSerYValAspAlaValPheThz 379
Db      2647 CGTCCAGAACCATTAATAGGCATCAATCAATAATTAATTAAGATGATGACGATATTCA 2706
Qy      380  ValAspThzrGLYmetCYuAsnValTPHNIaLEaArgTYrILEGLuAsnProGLUGLYThz 399
Db      2707 GCAATGTAGGTACACGACACAGTTTGGTCACTGAACTTA--AACCTTGGCTGAAT 2763
Qy      400  ArgAspPheValGLYSerPheArgNIaGLYThzMeAlaAsnAlaLeuProHIsAlaILE 419
Db      2764 AACAAATTCATCATTTCAAGTTGGTTAGTACATAGGGGTTCCGGCTTCCAGCGTCAATT 2823
Qy      420  GLYlaGLInSerValAspArgAsnArgGLInValILEaMetCYuSGILYAspGLYGLYLeu 439
Db      2824 GCATCAAAATATTCATATCCAAATAGACAAGCCATCCCAATTCGCTGGTGAACGGTGCATTC 2883
Qy      440  GLYmetLeuSeuGLYGLUleuLeuThzVallySeuHIsGLInLeuProLYuValaVal 459
Db      2884 CAATATGGTAATGACAAAGCTTCGCTACACGACTACAAATAGATTAATCTTTAATCTGATTT 2943
Qy      460  ValPheAsnAsnSerSerLeuGLYmetVallySeuGLUmetLeuValGLUGLYGLInPro 479
Db      2944 GTACTTTAATAACAACGTTAGCATTTATTAATAATGAACAACAAGCAGCTGGTGAATTA 3003
Qy      480  GLUthreGLYThzAspHIsGLUGluValaAsnPheAlaGLUleuAlaAlaAlaGLYILE 499
Db      3004 GAATATGACAGTGAATTTTCTGATATAGATCATCAAAATTTGCTGAGCAGCAGCTGCT 3063
Qy      500  LysSerValArgILEthAspProLYuValArgGLInLeuAlaGLUlaAlaLeuAla 519
Db      3064 AAAGGTTATACAAATTAAGAAGCTTACGCAAGATATAGCTATAGTGAAGAGGCAATTAGCA 3123
Qy      520  TYrProGLYProValleuLeaPHEValThzAspProAsnAlaLeuSerILEProPro 539
Db      3124 CAAGATGATCAACAGATTTGATGATGATATAGTTGATCTTAATGCTGGCCATTAACAAGT 3183
Qy      540  ThrILEthTrpGLUGluInValMetGLYPheSerlyAlaAlaThzArgThrVal 557
Db      3184 AAAATTGTAAATGAAGAAGCGCTGGTTATGTATGTATAGTGGCATTTAGATCAATT 3237

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Patent No. 6737248  
 GENERAL INFORMATION:  
 APPLICANT: Charles Kunsch  
 TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
 NUMBER OF SEQUENCES: 5255  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: Maryland  
 COUNTRY: USA  
 ZIP: 20850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
 COMPUTER: HP Vectra 486/33  
 OPERATING SYSTEM: MSDOS version 6.2  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/781,986A  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Benson, Bob  
 REGISTRATION NUMBER: 30,446  
 REFERENCE/DOCKET NUMBER: PB248PP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (301) 309-8504  
 TELEFAX: (301) 309-8512  
 INFORMATION FOR SEQ ID NO: 138:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7900 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 US-08-781-986A-138  
 Alignment Scores:  
 Pred. No.: 6,996-77 Length: 7900  
 Score: 790.50 Matches: 183  
 Percent Similarity: 52.69% Conservative: 111  
 Best Local Similarity: 32.80% Mismatches: 249  
 Query Match: 26.48% Indels: 16  
 DB: 4 Gaps: 8  
 US-09-965-825-2 (1-579) x US-08-781-986A-138 (1-7900)  
 QY 7 GluInleuileaspThrLeuGluAlaGlnIlyValIysArgIleTyrGlyLeuValGly 26  
 Db 1589 GAAGCATTAAGTTAAGATTACAGCATTCAGATTAAGATTCATCTGTATGATTCAGGA 1648  
 QY 27 AsperleuamPcollevalaspalaValArg-----GlnSeraspIleGluTyrVal 44  
 Db 1449 GACTCAATTCAGCGC-ATATGTCGATGATTAGTACAGTACAGATCATTAATTTAT 1707  
 QY 45 HisValArgangluGluAlaAlaPheAlaAlaGlyAlaGluSerleuIleThrgly 64  
 Db 1708 CATGTACGTATGATGAGAGAGTACAGAGCTTACGCGCTGCTGTACCAAAATTAATCTGCT 1767  
 QY 65 GluLeuAlaValCysAlaAlaSerCysGlyProGlyAsnThrHisleuIleGlnGlyLeu 84  
 Db 1768 AATATCGCTGTCATTAAGTATGCTGCGCTGCTGTTAATTCATTTATTAATGATG 1827  
 QY 85 TyrAspSerHisArganglyAlaIysValIleAlaIleAlaSerHisIleProSerAla 104  
 Db 1828 TATGATGCCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1887  
 QY 105 GlnIleGlySerThrPhePheGlnGluIleThrHisIleProGluIleLeuPheIleGlySer 124  
 Db 1888 GCACCTTGAAAGCAAGACATTCAGAGAAACAAATTTACAAATTAATGTAAGATGATGCC 1947

QY 125 GlyTyrCysGluMetValaIserGlyGluGlnGlyGluArgIleLeuHisIleAlaIle 144  
 Db 1948 GTTATATATCAACAAATTTGAAAAAGGTGACAAATGTTTAAATCGTTAAAGCAAGCAAT 2007  
 QY 145 GlnSerThrMetAlaGlyIysGlyValaIserValaValaIleProGlyAspIleAlaIys 164  
 Db 2008 CGTACGGATATGCAACAAAGGTGATGCTGTTGTTATTTGCTTAACGCTTATTAAC 2067  
 QY 165 GluAspAlaGlyAspGlyThrTyrSerAsnSerThrIleSerSerGlyThrPro--Val 183  
 Db 2068 GAAAAATTTAAGATACACG-----ATTAACCAAGATATCAACCAAGACCAACAGTA 2121  
 QY 184 ValPheProaspProthrGluAlaAlaIleValaGluAlaIleAsnAsnAlaIysSer 203  
 Db 2122 GTATCAACCAAAATTAAGATACACCAAAAGCGGTAACTAATTAATTAAGATTAAG 2181  
 QY 204 ValThrIleuPheCysGlyValaGlyValaIysAsnAlaArgAlaGlnValaIleuGluAla 223  
 Db 2182 CCTGTATGTTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2241  
 QY 224 GluIysIleIysSerProIleGlyHisAlaIleGlyGlyIysGlyIleGlnIleGln 243  
 Db 2242 GAATGCGTAAATTCCTGCTGATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 2301  
 QY 244 AspProPheGluValaGlyMetSerGlyLeuLeuGlyTyrGlyAlaCysValaAspAlaSer 263  
 Db 2302 CATCAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2361  
 QY 264 AsnGluAlaAspLeuIleLeuGlyThrAspPheProIysSerAspPheLeuPro 283  
 Db 2362 CAGGAGCGGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 2421  
 QY 284 IysAspAsnVal-----AlaGlnValaIleAsnGlyAlaHisIleGlyArgArgThr 301  
 Db 2422 AAGAAAAATTTAAGCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 2481  
 QY 302 ThrValIysTyrProValThrGlyAspValaAlaThrIleGluAsnIleLeuProHis 321  
 Db 2482 AATATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2541  
 QY 322 ValIysGlyIysThrAspArgSerPheLeuAspArgMetLeuIysAlaHisIleGlyArg 341  
 Db 2542 ATTAACAATGTTGCGAAGACCAATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 2592  
 QY 342 Leu-----SerSerValaIleGluThrTyrThrHisAsnValaGlyIysHisValaProIle 359  
 Db 2593 GCGGTTTGGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2646  
 QY 360 HisProGluTyrValaIleAlaSerIleLeuAsnGluLeuAlaAspIysAspAlaValaPheThr 379  
 Db 2647 CGTCCAGAACGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2706  
 QY 380 ValAspThrGlyMetCysAsnValaIleThrHisAlaArgTyrIleGluAsnProGluIleThr 399  
 Db 2707 GCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2763  
 QY 400 ArgAspPheValaGlySerPheArgHisIleGlyThrMetAlaAsnAlaLeuProHisAlaIle 419  
 Db 2764 AACAGTTATCATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2823  
 QY 420 GluValaGlnSerValaAspArgAsnArgGlnValaIleAlaMetCysGlyAspGlyGlyLeu 439  
 Db 2824 GCATCAAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2883  
 QY 440 GlyMetLeuLeuGlyGluLeuLeuThrValaIysLeuHisGlnLeuProLeuIysAlaVal 459  
 Db 2884 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2943  
 QY 460 ValPheAsnAsnSerSerLeuGlyMetValaIysLeuGluMetLeuValaGlnGlyIlePro 479  
 Db 2944 GATCTTAATTAACAAACAGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3003  
 QY 480 GluPheGlyThrAspHisGluGluValaIleAsnPheAlaGluIleAlaAlaGlyIle 499

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Db 3004 GAATATGAGTGTATTTCTGATATGATCATGCAAAATTTGGCTGAGCGAGCTGCT 3063
Qy 500 LysSerValArgIleThrAspProLysValArgGluGlnLeuAlaGluAlaLeu 519
Db 3064 AAAGGTTATACAAATAGAGTGTAGCGAGTGTAGTGTATGTAGTGAAGAGGATTCACA 3123
Qy 520 TyrProGlyProValLeuIleAspIleValThrAspProAlaLeuSerIleProPro 539
Db 3124 CAAGATGTACCAAGCATTTGTATGTATATGTATCTTATGTCTGAGCCCATTCACAGCT 3183
Qy 540 ThrIleThrProGluGlnValMetGlyPheSerIysAlaIleThrArgThrVal 557
Db 3184 AAATTTGAATGAAGAAAGCGCTGTATGTGTAAAGTGGCATTTAGATCAATT 3237

RESULT 10
US-09-134-001C-1619
/ Sequence 1619, Application US/09134001C
/ Patent No. 6380370
/ GENERAL INFORMATION:
/ APPLICANT: Lynn Doucette-Stamm et al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
/ FILE REFERENCE: GTC-007
/ CURRENT APPLICATION NUMBER: US/09/134,001C
/ PRIOR FILING DATE: 1998-08-13
/ PRIOR APPLICATION NUMBER: US 60/064,964
/ PRIOR FILING DATE: 1997-11-08
/ PRIOR APPLICATION NUMBER: US 60/055,779
/ NUMBER OF SEQ ID NOS: 5674
/ SEQ ID NO 1619
/ LENGTH: 1761
/ TYPE: DNA
/ ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1619

Alignment Scores:
Pred. No.: 2,19e-73 Length: 1761
Score: 749.50 Matches: 172
Percent Similarity: 50.98% Conservative: 114
Best Local Similarity: 30.66% Mismatches: 254
Query Match: 25.11% Indels: 21
DB: 3 Gaps: 9

US-09-965-825-2 (1-579) x US-09-134-001C-1619 (1-1761)
Qy 7 GluGlnLeuIleAspThrLeuGlnAlaGlnIlyValLysArgIleTyrGlyLeuValGly 26
Db 43 GAACATTTAGTTAAGGCTTACAAACCTGGAATATGTATCATTTATATGATTCCTGCGC 102
Qy 27 AspSerLeuAsnProIleValAlaAspAlaValArg-----GlnSerAspIleGluTrpVal 44
Db 103 GACCTAGAGATGCTGTGTGTATGATGCTTACGTACGTCAGAGATCAATTTAAATTCAT 162
Qy 45 HisValArgAsnGluGlnAlaAlaAspAlaGlnIleGlyAlaGlnSerLeuIleThrGly 64
Db 163 CACGTACGTCATGAAAGAGTACGAGTGTACCTGCTGCAAGTTACACAAATAATGACAGG 222
Qy 65 GluLeuAlaValCysAlaAlaSerCysGlyProGlyAsnThrHisLeuIleGlnIlyLeu 84
Db 223 AAAATTTGTGTAGCTTTAAGTATCGAGAGCTGTATGTATGACCTTTATTAAGGTATG 282
Qy 85 TyrAspSerHisArgAsnGlyAlaLysValLeuAlaIleAspSerHisIleProSerAla 104
Db 283 TACCATGTAAATAGGATTAATGTACTCTCACTTATTTATCTGGACAAACAAATAGTACA 342
Qy 105 GlnIleGlySerThrPhePheGlnGluThrHisProGluIleLeuPheLysGluCysSer 124
Db 343 TTATTAGGTACAAATTTCTTCCAAACAGCAAACTTTCTAAATGTTGATGATGTGCT 402
Qy 125 GlyTyrCysGluMetValAsnGlyGlyGlnGlnGluArgIleLeuHisAlaIle 144

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Db 403 GTATATGACCAACCAATTCAAAAAGTGTATACGTAATTTGAAATTAACAATGACCAATT 462
Qy 145 GlnSerThrMetAlaGlyLysGlyValSerValValIleProGlyAspIleAlaLys 164
Db 463 GTTACGGCATACGAGAAAAAGGTGTCTCTGTATTCATTTGTCCAAATGACTTTTAACT 522
Qy 165 GluAspAlaGlyAspGlyThrTyrSerAsnSerThrIleSerSerGlyThrPro----- 182
Db 523 CAATAATTTAAAGACATGAC-----AATGTGACGTGTATACAACTTAACCAAAACCA 576
Qy 183 -----ValValPheProAspProThrGluAlaAlaLeuValGluAlaIleAsnAsn 200
Db 577 GCTTACCAACCAAAATTCAAAGATTTAAAAAAGCAGCTTAATTA-----ATTGATTA 627
Qy 201 AlaLysSerValThrLeuPheCysGlyValGlyValLysAsnAlaArgAlaGlnValLeu 220
Db 628 GCTAAACCAAGTAATGCTTATTTGTTAGTACACACGCTTAAGATGAATTAAGCT 687
Qy 221 GluLeuAlaGluLysIleLysSerProIleGlnHisAlaLeuGlyGlyLysGlnTyrIle 240
Db 688 GAATTTATGAAAGTGTCAAAAAATTCAGTTATTCACATTAACCTGCAGAAAAACATCTTA 747
Qy 241 GlnHisGluAsnProPheGlnValGlyMetSerGlyLeuGlyTyrGlyAlaCysVal 260
Db 748 CCGACCATCATCTTATAGTATGTATGTAAGTAAATGTTAAATGTTAAACATCTTAT 807
Qy 261 AspAlaSerAsnGlnAlaAspLeuLeuIleLeuLeuGlyThrAspPheProTyrSerAsp 280
Db 808 CAACCAATTCAGATGACAGACTTATTAATTAATGCTGTACGAACTATCCCTATGTTAAC 867
Qy 281 PheLeuProLysAspAsnVal-----AlaGlnValAspIleAsnGlyAlaHisIleGly 298
Db 868 TATTACTTAAGAAATTAACATTAAGCTATTCATTCATTCAGAACGAAAGAAATATTCGT 927
Qy 299 ArgArgThrThrValLysTyrProValThrGlyAspValAlaAlaThrIleGluAsnIle 318
Db 928 GCACGCTTAAATTAATGATGTATTTAGTATGATGTAAGTGTCTTCATCACTA 987
Qy 319 LeuProHisValLysGluLysThrAspArgSerPheLeuAspArgMetLeuLysAlaHis 338
Db 988 ACTGAAACCAATTAAGCATGTGCAAAAGTCCATTTAGATGAAGACATTA----- 1038
Qy 339 GluArgLysLeuSerSerValAlaGluThrThrHisAsn-----ValGluLysHis 356
Db 1039 GAACGTAAA-----GCAGTTGGGATTAATGATGATGAACAAAGTTGAATTAAGCAAT 1092
Qy 357 ValProIleHisProGluTyrValAlaLaserIleLeuAsnGlnLeuAlaAspLysAspAla 376
Db 1093 TCACCATTTAGCTCCAGAACGTTTAATGAAGCATCAATGTAATTAAGATGATGCA 1152
Qy 377 ValPheThrValAspThrGlyMetCysAsnValIlePheAlaArgTyrIleGluAsnPro 396
Db 1153 ATTATTCACAGAGATGTGTGTACTTCAAGTATGCTACGCGCTTACTTA---AACTTA 1209
Qy 397 GluLysThrArgAspPheValGlySerPheArgHisGlyThrMetAlaAsnAlaLeuPro 416
Db 1210 TCTGTAAATTAATTAATTCATTTATTTAGTTGTTAGTATGAGCTGTGCTGTTTACA 1269
Qy 417 HisAlaIleGlyAlaGlnSerValAspArgAsnArgGlnValIleAlaMetCysGlyAsp 436
Db 1270 GGTGCGATGCGGATTAATTTGCTTATTCACAAACGTCAGAGAGTATGATACAGGGTAC 1329
Qy 437 GlyGlyLeuGlyMetLeuLeuGlyGlnLeuLeuThrValLysValHisGlnLeuProLeu 456
Db 1330 GGTGCGTTCACAAATGATATGCAAGACCTTGTCACTGTTCACATTAATTACTTCAATG 1389
Qy 457 LysAlaValValPheAsnAsnSerSerLeuGlyMetValLysValLysLeuGlyMetLeuValGlu 476
Db 1390 ACAATCTTCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1449
Qy 477 GlyGlnProGluPheGlyThrAspHisGlyGluValAspPheAlaGluIleAlaAla 496
Db 1450 GGTGAATTAAGTATGCAATTTGTTCTGATATGATCATGCTAAATTTGCGAAGCT 1509

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QY 497 AlIGlyIleYserValArgIleThrAspProLYsValArgIleuAlaGlu 516  
 Db 1510 GCTGGGTAAAGCATATGTTGCAAGATGTAAGTCCTTGACAACATCGTGAAGG 1569  
 QY 517 AlAlenAlaTYrProGlyProValLeuIleAspIleValThrAspProAlaLeuSer 536  
 Db 1570 GCATGGCTCAAGATGTTCCACATCGTTGACGTTGATCTTAATGCTGACCA 1629  
 QY 537 IleProThrIleThrIleThrIleValMetGlyPheSerIleAlaIleThrArgThr 556  
 Db 1630 TTAACGATTAATTTGTAACAGAGACATTTGGTTACATTAATGGGCTTAATGATCA 1689  
 QY 557 Val 557  
 Db 1690 ATT 1692

RESULT 11  
 US-09-252-991A-8458  
 / Sequence 8458, Application US/09252991A  
 / Patent No. 6551795  
 / GENERAL INFORMATION:  
 / APPLICANT: Marc J. Rubenfield et al.  
 / TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 / TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 / FILE REFERENCE: 107196.136  
 / CURRENT APPLICATION NUMBER: US/09/252,991A  
 / PRIOR FILING DATE: 1999-02-18  
 / PRIOR APPLICATION NUMBER: US 60/074,788  
 / PRIOR FILING DATE: 1998-02-18  
 / PRIOR APPLICATION NUMBER: US 60/094,190  
 / PRIOR FILING DATE: 1998-07-27  
 / NUMBER OF SEQ ID NOS: 33142  
 / SEQ ID NO 8458  
 / LENGTH: 2577  
 / TYPE: DNA  
 / ORGANISM: Pseudomonas aeruginosa  
 / US-09-252-991A-8458

Alignment Scores:  
 Pred. No.: 1,49e-72 Length: 2577  
 Score: 744.50 Matches: 191  
 Percent Similarity: 51.85% Conservative: 104  
 Best Local Similarity: 33.57% Mismatches: 241  
 Query Match: 24.94% Gaps: 33  
 Indels: 13

US-09-965-825-2 (1-579) x US-09-252-991A-8458 (1-2577)  
 QY 1 MetAlaHisSerTYrAlaGluIleuIleAspThrIleuAlaIleGluValIleValArg 20  
 Db 805 ATGCCAGCAAGCTGGTCCGATCAATTCCTCAACCTTGAGCCAGTGGGGTGAAGCC 864  
 QY 21 IleTYrGlyLeuValGlyAspSerLeuAsnProIleValAspAlaVal-----ArgIle 38  
 Db 865 GTCTTCGGCTAACCCAGCGCATGCGATCAACGGGATCATGGCGCCGCGCCGCCGCC 924  
 QY 39 SerAspIleGlyTrpValHisValArgAsnGluAlaAlaIleAlaIleAlaIleAla 58  
 Db 925 GAGGCAATTCACATATATCCGCGTCCGCGCAGAGAAATGGCGGCTTCATGGCGCGCC 984  
 QY 59 GluSerIleuIleThrGlyGluLeuAlaValCysAlaIleSerCysGlyProGlyAsnThr 78  
 Db 985 CACGCCAATTCACCGGAGAGTCCGGGTGTGCTGCCACCTCGGGGCGCGGCGGATC 1044  
 QY 79 HisLeuIleGlnIleuTYrAspSerHisValArgAsnGlyAlaIleValIleAlaIleAla 98  
 Db 1045 CACTCTCTGAACGCGCTTAACAGACGCCCATGATCATCAACCGGTGTGCGCATCGTC 1104  
 QY 99 SerHisIleProSerAlaGlnIleGlySerThrPhePheGlnGluThrHisProGluIle 118  
 Db 1105 GGCCACAGCGCGCTACCGGTTGGCAGCGATCAACAGAGAAATGTCATCTGACAGGC 1164

QY 119 LeuPheIleGlyCysSerGlyTYrCysGluMetValAsnGlyGlyGlnGlyGluArg 138  
 Db 1165 TTGTCAAGAGCATTTCCGCTTATGTCAGACCGTGTGACCGCCGACAACTGCTCAT 1224  
 QY 139 IleLeuHisAlaIleGlnSerThrMetAlaGlyIleGlyValIleSerValIleValIle 158  
 Db 1225 GTGCTGACCAAGAGCTCGCGCGTGGCGGCGGAGGCGGAGGTGGCGACGTTGATCGTG 1284  
 QY 159 ProGlyAspIleAlaIleGlyAspAlaGlyAsp---GlyThrTYrSerAsnSerThrIle 177  
 Db 1285 CCCAACACGTCGCAACAGATGGCGGCCGGAAGCGCAAGCCCAACAGACAGCCACGTCG 1344  
 QY 178 SerSerGlyThrProValIlePheProAspPro-----ThrGluAla 191  
 Db 1345 ATGTGGCGGTGGCTTGTGTCAGCCGACCTTAACGCGCGGACCCGACCTGAGGCGC 1404  
 QY 192 AlaAlaLeuValGluAlaIleAsnAlaIleValSerValIleThrLeuPheCysGlyAlaGly 211  
 Db 1405 GCCGCGCGCATC-----CTCAATCCGCGCGCGCGCGTGCATCTCGCGGTGCGGC 1458  
 QY 212 ValIleAsnAlaArgAlaGlnValIleuGluLeuAlaGluIleYserProIleGly 231  
 Db 1459 GCCCTGGCGCGACCGGCAACTGAAGCGGTGCGGACGCGCTGGCGCGGAGTGCGC 1518  
 QY 232 HisAlaLeuGlyIleGlyGlnTYrIleGlnHisGluAsnProPheGluValIleMetSer 251  
 Db 1519 AAGCGCTCTCGGGCAAGCGCGGCTTCCGACGACCTGCTAGCTGACCGCTTCATC 1578  
 QY 252 GlyLeuLeuGlyTYrGlyValCysValAspAlaSerAsnGluAlaAspLeuIleLeu 271  
 Db 1579 GGCTGCTCGGACCGCGCGACGATGATGAGACATTTGGACACCTGCTGATC 1638  
 QY 272 LeuGlyThrAspPheProTYrSerAspPheLeuProLYsAspAsnValAla----- 288  
 Db 1639 GTCGGACGACTTCCCTCAACGAGATCTTAACCAAGCGCGCGCGCGCGGTG 1698  
 QY 289 GlnValAspIleAsnGlyValHisIleGlyArgTYrThrValIleTYrProValIleThr 308  
 Db 1699 CAGATGACCTGTATCCGCGGCAACATCGGTATCCGTTATCCGATGACCAAGCCTTGCTC 1758  
 QY 309 GlyAspValAlaIleThrIleGluAsnIleLeuProHisValIleGlyValIleAspArg 328  
 Db 1759 GCGGATGCAAGGAAACCTTGAGCGCTGCGCTGCGTGCAGCAAAAGACAGCGC 1818  
 QY 329 SerPheLeuAspArgMetLeuValHisIleGlyArgIleYserSerValIleGluThr 348  
 Db 1819 GCTGCGCGCGCGCGCTC-----GAGCGGCGCGTGGACGCGCATGCGGAGAA 1866  
 QY 349 TYrThrHisAsnValGluIleHisVal---ProIleHisProGluTYrValAlaIleSerIle 367  
 Db 1867 GCCCGCGCGCAGCGCGGAGAGCCAGCCGACCGCATCAACCGCGCGGTATTCGTTCC 1926  
 QY 368 LeuAsnGluLeuAlaAspIleAspAlaValPheThrValAspThrGlyMetCysAsnVal 387  
 Db 1927 TTGTGGAGCACTGCCGCGAGATGCGATTCCTCGCGGCAACGCGCTCGCATACCAAC 1986  
 QY 388 TrpHisAlaArgTYrIleGluAsnProGluIleTYrThrArgAspPheValIleYserPhe--- 406  
 Db 1987 TGTGACGCGCGGACATCCGATCCGCGCGCGG-----ATGCTCGGCTGCTGCTG 2037  
 QY 407 ---ArgHisGlyThrMetAlaAsnAlaLeuProHisAlaIleGlyAlaGlnSerValAsp 425  
 Db 2038 GGCAGAGCTGGGACCAATGGGACGCGGTGCTCCCTTAACCTCCGCGCAAGCTCGCTAT 2097  
 QY 426 ArgAsnArgIleValIleAlaMetCysGlyIleGlyIleuIleMetLeu---LeuGly 444  
 Db 2098 CCGGACGCGCGCGGTGGTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2157  
 QY 445 GluLeuLeuThrValIleValIleHis-----GlnLeuProLeuValAlaVal 459  
 Db 2158 GAATGCTGACCGGACGAGTACTGGACGCGGTGGGACTCGCGCACTTCACTGCTGCTG 2217  
 QY 460 ValPheAsnAsnSerSerLeuGlyMetValIleLeuGluMet---LeuValGluGln 478



QY 460 ValPheAsnAsnSerSerLeuGlyMetValIysLeuGluMet---LeuValGluGlyGln 478  
DB 2084 GTGGTGAACAAACGGGATCTCAACAGAGGACCTGGAGACAGCGCCCTGGCCGCGAC 2143  
QY 479 ProGluPheGlyThrAspHisGluGluValAspPhe-----AlaGluIleAlaAla 496  
DB 2144 CCGGAGTTCAGCCCGCGGACAGATGATTCATTCCTTACGCGCGTATATGCGACATG 2203  
QY 497 AlaGlyIleLysSerValArgIleThrAspProLysLysValArgGluGluLeuAlaGlu 516  
DB 2204 CTGGCTTCAGAGGATCGCGTGGATCGCCGAGAGACATGACGCGCCCTGGGCGGAG 2263  
QY 517 AlaLeuAlaIyrProGlyProValIleuIleAspIleValIThrAspProAlaIleuSer 536  
DB 2264 GCTTCGCGCGCGACCGCCGCGTGTCTGTGAGAGTGTCAACGACCGGAGTGCCTCCG 2323  
QY 537 IleProProThrIleThrTrpGluGln 545  
DB 2324 CTGCGCGCGACATCATGTTTCGAGCAG 2350

RESULT 13  
US-09-252-991A-7281/c  
; Sequence 7281, Application us/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 7281  
; LENGTH: 1113  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-7281

Alignment Scores:  
Pred. No.: 2.07e-67 Length: 1113  
Score: 693.00 Matches: 142  
Percent Similarity: 61.94% Conservative: 81  
Best Local Similarity: 39.44% Mismatches: 129  
Query Match: 23.22% Indels: 9  
DB: 4 Gaps: 4

US-09-965-825-2 (1-579) x US-09-252-991A-7281 (1-1113)

QY 6 AlagluGluIleuIleAspThrLeuGluAlaGluGlyValIysArgIleTyrGlyLeuVal 25  
DB 1059 GCGGAGATCTCTGCGAAACCTTGGAGCGCGCGCGTCCGCCATTGCTATGCGCATCGTC 1000  
QY 26 GlyAspSerLeuAsnProIleValAspAlaValArgGlnSerAspIleGluTrpValHis 45  
DB 999 GGGGACACCTTCAACATGTCACCGAGCGCATTCATCGAGCGACATTCAGTGGGTCCAC 940  
QY 46 ValArgAsnGluGluAlaAlaPheAlaAlaGlyAlaGluSerLeuIleThrGlyGlu 65  
DB 939 GTGCGGACCAAAACCGGCGCTTCGCGCGCGCGCGAGTCTTACATCAGCGGACGCG 880  
QY 66 LeuAlaValCysAlaIleSerCysGlyProGlyAsnThrHisLeuIleGluIleuTyr 85  
DB 879 CTGACCGCGCTCGCGCGCTCTCTCGGACCGGCGAGCTTCACTTCAACAGCGGTAC 820  
QY 86 AspSerHisArgAsnGlyAlaIysValLeuAlaIleAlaSerHisIleProSerAlaGln 105  
DB 819 GAGGCCACAGCGGACCGCGGATGCTGATGCGACGACAGATGCTTACCCCGCA 760

QY 106 IleGlySerThrPhePheGluGluThrHisProGluIleLeuPheLysGlyCysSerGly 125  
DB 759 CTGGGATGAGATTTTCCCGAGAGGTGACTTCAAGGCGGTCTTACAGCGCTCTGCTG 700  
QY 126 TyrCysGluMetValAsnGlyGlyGluGlnGlyIleuArgIleLeuHisIleAlaIleGln 145  
DB 699 TTCTGCGAGAGGTGACACCGCGGACAGCGCGCGCGGTGTGTCGCTGCGCTGCGCAG 640  
QY 146 SerThrMetAlaGlyLysGlyValSerValValIleProGlyAspIleAlaIysGlu 165  
DB 639 GCGCGCTCAACCGGCGCGCGGTGTGTATCTGCTGCGCGGACATCAGCCAGGCG 580  
QY 166 AspAlaGlyAspGlyThrTyrSerAsnSerThrIleSerSerGlyThrProValAlaPhe 185  
DB 579 ACGGTGAAGACACCTG-----CGTTCTGCTGCAATTTCCCGAACCGGTGCGC 526  
QY 186 ProAspProThrGluAlaAlaValAlaGluAlaIleAsnAsnAlaLysSerValThr 205  
DB 525 CCCAGCGACCGGACCTGCGAGAGCTGCGCGCGCTGCTGCGCGACGGAAGATCGGC 466  
QY 206 LeuPheCysGlyAlaGlyValIysAsnAlaAlaGlnValLeuGluIleuAlaIys 225  
DB 465 ATCTAGCGCGCTCGCGCTGCGAGGCGCCACAGACTGTGTGCTGCTGCGCGCGC 406  
QY 226 IleLysSerProIleGlyHisAlaLeuGlyGlyLysGlnTyrIleGluHisGluAsnPro 245  
DB 405 CTGAGCGCCCATTCGCGACACGTGCGCGCGCGCGCGAGACTTGTGTGATGACACACCC 346  
QY 246 PheGluAlaGlyMetSerGlyLeuLeuGlyTyrGlyAlaCysValAspAlaSerAsnGlu 265  
DB 345 TTCAATGAGGATGACCGGTATGCTCGGAGATGAGTCCGCGCTTCCATGATGACCGAG 286  
QY 266 AlaAspLeuIleuIleuGlyThrAspPheProTyrSerAspPheLeuPro---Lys 284  
DB 285 TGGACACCTCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 226  
QY 285 AspAsnValAlaGluValAspIleAsnGlyAlaHisIleGlyArgArgThrThrValLys 304  
DB 225 GCCACCTGATCAGGTGACCGGACGATGACCTGCGCGCGCGCGCGCGCGCGCGCGCG 166  
QY 305 TyrProValThrGlyAspValAlaAlaThrIleGluAsnIleLeuProHisValIysGlu 324  
DB 165 CTGGCGGTGCGGAGCGT-----ATCCC-CAGCTTGTCCGCTGCTGACAGCC 116  
QY 325 LysThrAspArgSerPheLeuAspArgMetLeuLysAlaHisGluAlaLysSerSer 344  
DB 115 CCGGAGAGCGGACCTTCTCTGACGAATGCTGGAGACCGCGAGCGCTGCGGAGCG 56  
QY 345 ValValGluThrTyrThrHisAsnValGluLysHisValProIleHisProGluTyrVal 364  
DB 55 CTGGAATAA-----GAGGAGCAAGCGCGGACGCGATGATCATTCCGACGACCTG 2

RESULT 14  
US-09-252-991A-7413  
; Sequence 7413, Application us/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 7413  
; LENGTH: 1083  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-7413

## Alignment Scores:

Pred. No.:	1.2e-66	Length:	1083
Score:	686.00	Matches:	138
Percent Similarity:	63.05%	Conservative:	77
Best Local Similarity:	40.47%	Mismatches:	120
Query Match:	22.98%	Indels:	7
DB:	4	Gaps:	3

US-09-965-825-2 (1-579) x US-09-252-991A-7413 (1-1083)

```

Qy 6 AlaGlutInLeuIleAerThLeuGlUaIaGInGlyValIyAaGIlleTyGlyLeuVal 25
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 43 GCCAGATGCTGCGGAACCTGGAGACCGCGCGCTGCCATTCGATGCTATGGCATCTCC 102
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 26 GlYAsPserLeuAnProIleValAspAlaValArgInSerAerPleIleGluTrpValHis 45
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 103 GCGACACCTTCACATGTCACGACCGCATTCATTCGACGCGAGATCCAGTGGGTCCAC 162
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 46 ValArgAnGluGluValAlaAlaPheAlaAlaGlyAlaGluSerLeuIleThrGlyGlu 65
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 163 GTGGGCCACGAAGAAGCGCGCTTCGCGCGCGCGCGAGTCTATACATACGCGAGCC 222
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 66 LeuAlaValCyAlaAlaSerCyGlyProGlyAerThrHisLeuIleGInGlyLeuTy 85
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 223 CTGACCGCTGCGCGCTCTCTGCGAGCGGCGAGCTGCATTCATCAACGCGGTTCAC 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 86 AsPserHisArgAnGlyAlaIyValLeuAlaIleAlaSerHisIleProSerAlaGln 105
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 283 GAGGCCACGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 342
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 106 IleGlySerThrPhePheGInGluThrHisProGluIleLeuPheGlyGluCySerGly 125
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 343 CTGGGCAATGAGATTCTCCAGAGGTGCATTCAAGGCGGTTCAGCGCATCGCTCGGTG 402
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 126 TyrCyGluMetValaGInGlyGluGInGlyGluArgIleLeuHisIleAlaIleGln 145
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 403 TTCTGCGAGGAGTGCACAGCGCGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCG 462
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 146 SerThrMetAlaGlyValaSerValValIleProGlyAerPleIleAlaIleGlu 165
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 463 GCGGCGCTCAACCGCGCGCGGTGTGTGATCCGCGCGCGCATCGACAGCGCGCC 522
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 166 AsPAlaGlyAerGlyThrTySerAerSerThrIleSerSerGlyThrProValPhe 185
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 523 ACGGTGAAGACGACCTG-----CCGTTCTCGGTGCATTCCCGCAACCGGTCTCGCC 576
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 186 ProAerProThrGluAlaAlaAlaLeuValaIleAerAerAlaIySerValThr 205
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 577 CCCAGCGACGCGCAATGCGAGACGTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCG 636
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 206 LeuPheCyGlyAlaGlyValaIyAerAerAlaArgAlaGlnValaIleGluLeuAlaGlu 225
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 637 ATCTACGCGCGCTCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 696
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 226 IleTySerProIleGlyHisAlaLeuGlyGlyGlnTyIleGlnHisGluAerPro 245
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 697 CTCAAGGCGCGCATGCGCGACACGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 756
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 246 PheGluValaGlyMetSerGlyLeuLeuGlyTyIleGlyAlaCyValaIleAerAlaSerAerGlu 265
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 757 TTCAACATGGCGCATGACCGGTATGCTCGGATCGAGTCCGCGCTTCACATATACGAG 816
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 266 AlaAerLeuLeuIleLeuGlyThrAerPheProTySerAerPheLeuPro--Lys 284
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 817 TGCCACACCTCTCGGTGCTGCGCGCGCATTCGCGCGCGCGCGCGCGCGCGCGCG 876
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 285 AsPserValaIleGlnValaIleAerPleAerGlyAlaHisIleGlyArgAerThrValaIys 304
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 877 GCGACCTGATCGAGTGCAGCGCGGATGCGAGTCACTGCGCGCGCGCGCGCGCGCAT 936
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 305 TyrProValThrGlyAerValaAlaAlaThrIleGluAerIleLeuProHisValaIleGlu 324
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 937 CTGCGCGGTGTCGCGACGTC-----ATCCC-CAGCTCTTCCGCTGCTCGAAGCC 986
Qy 325 LysThrAerAerSerPheLeuAerAerMetLeuValaHisGluArgIyLeuSerSer 344
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 987 GCGGAGAGCGCGACCTTCTTCAGCAATGCTTGAGACGCGCGAGCGCTCGCTCGGACG 1046
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 345 Val 345
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1047 CTG 1049

```

## RESULT 15

US-09-107-532A-3181

Sequence 3181, Application US/09107532A

Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESSER: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: PC

OPERATING SYSTEM: &lt;Unknown&gt;

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Arinello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 3181:

SEQUENCE CHARACTERISTICS:

LENGTH: 1746 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHEICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...1746

SEQUENCE DESCRIPTION: SEQ ID NO: 3181:

US-09-107-532A-3181

## Alignment Scores:

Pred. No.:	1.66e-61	Length:	1746
Score:	643.00	Matches:	159
Percent Similarity:	49.55%	Conservative:	117
Best Local Similarity:	28.55%	Mismatches:	259
Query Match:	21.54%	Indels:	22
DB:	4	Gaps:	9

US-09-965-825-2 (1-579) x US-09-107-532A-3181 (1-1746)

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QY 9 LeuIleAspThrLeuGluAlaGlnGlyValIysArgIleTyrglyLeuValGlyAspSer 28
Db 43 ATGGTAAAGTTCTTGAAGCTGGGGTATCGACATATTTCACGGATCCCGAGAGATCT 102
QY 29 LeuAsnProIleValAspAlaValArgGln-----SerAspIleGluTrpValHisVal 46
Db 103 TTCATTCAATTATGATGCGCTATATCAAGAAAAAACCAAAATCACTCAATTCAGATT 162
QY 47 ArgAsnGluGluAlaAlaIlePheAlaIleGluSerLeuIleThrGlyGluLeu 66
Db 163 CGTATGAAAGAGTGGGCGCACTCGCACCCGCTGACAGATCAAAATTAACGGGAAATC 222
QY 67 AlaValCysAlaAlaSerCysGlyProGlyAsnThrHisLeuIleGlnGlyLeuTyAsp 86
Db 223 GAGCGTGTCTCGGCTGCGAGAACCTGGTCGACACATTGATCAATGATGTTGATGAT 282
QY 87 SerHisArgAsnGlyAlaIleValLeuAlaIleAlaSerHisIleProSerAlaGlnIle 106
Db 283 GCAAGATGACCAATGCTGCTAGTACGCTTTAGACAAAGTTGCTTCAATCCATG 342
QY 107 GlySerThrPhePheGlnGluThrHisProGluIleLeuPheLysGluCysSerGlyTy 126
Db 343 AACATTAACCTTTTCCAGAACTAAATGAATAATCTATTTCGACAGATGTTAGCGTATC 402
QY 127 CysGluMetValAsnGlyGlyGlnGlnGlyGluArgIleLeuHisAlaIleGlnSer 146
Db 403 AATGTCACAGTCATGACACCAAAAGTCTCCGATGATGATGAAGCCATTAAGCC 462
QY 147 ThrMetAlaGlyLysGlyValSerValValIleProGlyAspIleAlaLysGluAsp 166
Db 463 GCCATGACACTTAAGGGGCTATGCTGACTGATCCCTGATGATCTGTTTGAAGAA 522
QY 167 AlaGlyAspGlyThrTySerAsnSerThrIleSerSerGlyThrProValAlaPhePro 186
Db 523 ATTGACGAACAACCTTCTCCACCGCTCAC---ACTGCAAAACAAAGTGATTTTCCA 579
QY 187 AspProThrGluAlaAlaAlaLeuValGluAlaIleAsnAsnAlaLysSerValThrLeu 206
Db 580 GAAGAAAAAGATGTTGCTAGCTGCTTGCCTTATCTTGAAGAAAAAACCAAGTCTT 639
QY 207 PheCysGlyAlaGlyValLysAsnAlaArgAlaGlnIleLeuGluMetAlaGlyLysIle 226
Db 640 TATCTTGGTCAAGAAAGCGAAACGAAATTCGCCGAATTCAAAGATCTCAAGAACATTT 699
QY 227 LysSerProIleGlyHisAlaLeuGlyGlyLysGlnTyrlleGlnHisGluAsnProPhe 246
Db 700 TCACTTCTGTTGCTGCTCCGTTCTAGCAAAAGAAATTAATTCCTGATGATTAAGAAAC 759
QY 247 GluValGlyMetSerGlyLeuLeuGlyTyrglyAlaCysValAspAlaSerAsnGluAla 266
Db 760 TTTCTTGGTGTTCGTCAGCGTGCCTACTTAACCCGGAATGAAAGCATTGCGCAAGGCC 819
QY 267 AspLeuLeuIleLeuLeuGlyThrAspPheProTy-----SerAspPheLeuProLys 284
Db 820 GATCTGATCTTATTTGCGTAGCGACTTCCTCATTTGACGCTGATTTTAAATCCAAT 879
QY 285 AspAsnValAlaGlnValAlaPheIleAsnGlyAlaHisIleGlyArgArgThrValLys 304
Db 880 GCTGAATTTATCCAAATCGATATCGATGCGTCAAAATTTGACAGCGCCATGAACATCT 939
QY 305 TyrProValThrGlyAspValAlaAlaThrIleGluAsnIleLeuProHisValLysGlu 324
Db 940 TTTGTCGATCTCGGTGATGCAACACACAGCTTGCAGAACCTGTCTC-----GAG 987
QY 325 LysThrAspArgSerPheLeuAspArgMetLeuLysAlaHisGlu-----ArgLys 341
Db 988 TTAGGGGATCTGCGCTGCTGATAGCTGATCTTACCAATCAAGAAATTAAGAAAAA 1047
QY 342 LeuSerSerValValGluThrTyrlleHisAsnValGluLysHisValProIleHisPro 361
Db 1048 TGGGTAAATGTTGAATCTTTTGAAGATCGAAGAGAAAGAA-----CGATTCGTCCA 1101
QY 362 GluTyValAlaSerIleLeuAsnGluLeuAlaAspLysAspAlaValPheThrValAsp 381

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Db 1102 GAGGCTGTCTATAAAGAAATCAATCGATTTGCTGAAGACATCGATTTTGTGCACAGAT 1161
QY 382 ThrGlyMetCysAsnValThrPheAlaArgTyrlleGluAsnProGluGlyThrArgAsp 401
Db 1162 GTGCTGACACAGACTAC---CATTTCAATTCGTTATGTAATGCAACGGTAAACAAAA 1218
QY 402 PheValGlySerPheArgHisGlyThrMetAlaAsnAlaLeuProHisAlaIleGlyAla 421
Db 1219 CATACGATCTTGATGCTTCGCAACTATGAGTAAATGCTGTGCTGAGAGAAATTCGCCGA 1278
QY 422 GlnSerValAspArgAsnArgGlnValIleAlaMetCysGlyAspGlyLysGlyMet 441
Db 1279 CAACTAAGTACCAAGAAACAAAGATATTACCTTAAGTGTATGATGCGGGTTGCTATG 1338
QY 442 LeuLeuGlyLysLeuLeuThrValLysLysHisGlnLeuProLeuLysAlaValPhe 461
Db 1339 GTCATGCAAGATTCATTTACACAAAGTCMAATATACCTTCCATTTATATGTTGCTTT 1398
QY 462 AsnAsnSerSerLeuGlyMetValLysLeuGluMetLeuValGluGlnProGluPhe 481
Db 1399 TCGAATGATCTTTTGGTTTCATCGAAGCAACAAAGAAATTCGGAACAAAGAAATTT 1458
QY 482 GlyThrAspHisGluGluValAsnPheAlaGluIleAlaAlaAlaGlyLysSer 501
Db 1459 GGTGATATTTTGAAGATGCAAGATTCGTTAAAGTTGGAAGAGCGCTCGGGCAATATAG 1518
QY 502 ValArgIleThrAspProLysValArgGluGlnLeuAlaGluAlaLeuAlaTyrllePro 521
Db 1519 TTTACGTCACAGAAATATCGCAACTGCAATTTGCTTGTGATGCACTCCAAATTCAGAT 1578
QY 522 GlyProValLeuIleAspIle---ValThrAspProAsnAlaLeuSerIle----- 537
Db 1579 CGTCCGTGATATCATGTGAAGATCAATTAACAGCCCATTCGCAGTGAAGATCTG 1638
QY 538 -----ProProThrIleThrTyrlleGluGlnValMetGlyPheSerLys 551
Db 1639 CATTTAGATCCAAAGAAATATCTGAAAGAAATCAAGCATTCAAAGAA 1689

```

Search completed: January 15, 2005, 15:01:39  
 Job time : 217 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: January 15, 2005, 14:12:37 ; Search time 880 Seconds

(without alignments)  
3780.533 Million cell updates/sec

Title: US-09-965-825-2

Perfect score: 2985

Sequence: 1 MAHSYARQLDITLRAQGVKR.....GGVGMIDLARSNIRNIPTP 579

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPRO.spool/US09965825/runat_14012005_093023_10355/app.query.fasta.1.775
-DB=Published Applications_NA -OPMT=faetap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Blomum62
-TRANS=numan40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09965825 @CGN 1.1 627 @runat_14012005_093023_10355
-NCRP=6 -ICPU=3 -NO MMAP -LARGEBUERT -NEG SCORES=0 -WAIT -DSPLOCK=100
-LOGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Database : Published Applications\_NA:\*

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2:	/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6:	/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8:	/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9:	/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10:	/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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17:	/cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18:	/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
19:	/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
20:	/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
21:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2985	100.0	1737	9 US-09-738-626-2873	Sequence 85, App1
2	2985	100.0	1860	17 US-10-781-014-85	Sequence 1, App1
3	2985	100.0	2160	9 US-09-965-825-1	Sequence 3, App1
4	2985	100.0	2160	15 US-10-143-856-3	Sequence 4, App1
5	2985	100.0	2160	15 US-10-078-167-4	Sequence 4, App1
6	2985	100.0	2160	15 US-10-336-049-4	Sequence 4, App1
7	2985	100.0	2160	15 US-10-091-142-4	Sequence 4, App1
8	2985	100.0	2160	15 US-10-686-736-4	Sequence 4, App1
9	2985	100.0	3248	9 US-09-965-825-4	Sequence 1, App1
10	2985	100.0	3309400	9 US-09-738-626-1	Sequence 17635, A
11	2300.5	77.1	1734	16 US-10-282-122A-17635	Sequence 2067, Ap
12	1746	58.5	1740	16 US-10-156-761-2067	Sequence 1, App1
13	1746	58.5	9025608	15 US-10-156-761-1	Sequence 89, App1
14	1590	53.3	944	17 US-10-781-014-89	Sequence 3, App1
15	1518	50.9	875	9 US-09-965-825-3	Sequence 5, App1
16	1518	50.9	875	15 US-10-143-856-5	Sequence 6, App1
17	1518	50.9	875	15 US-10-078-167-6	Sequence 6, App1
18	1518	50.9	875	15 US-10-336-049-6	Sequence 6, App1
19	1518	50.9	875	15 US-10-091-142-6	Sequence 6, App1
20	1518	50.9	875	15 US-10-686-736-6	Sequence 6, App1
21	1367	45.8	1716	16 US-10-282-122A-33768	Sequence 33768, A
22	1338	44.8	1722	16 US-10-282-122A-32583	Sequence 41795, A
23	1336	44.8	1722	16 US-10-282-122A-41795	Sequence 6012, Ap
24	1317.5	44.1	1719	9 US-09-815-242-6012	Sequence 1, App1
25	1317.5	44.1	1719	13 US-10-096-571-1	Sequence 1, App1
26	1317.5	44.1	1719	14 US-10-076-416-1	Sequence 20313, A
27	1317.5	44.1	1719	16 US-10-282-122A-20313	Sequence 12285, A
28	1316.5	44.1	1737	16 US-10-282-122A-12285	Sequence 23384, A
29	1309.5	43.9	1716	16 US-10-282-122A-19600	Sequence 19600, A
30	1298.5	43.5	1706	16 US-10-282-122A-19600	Sequence 9898, Ap
31	1285.5	43.1	1719	9 US-09-815-242-9898	Sequence 39776, A
32	1285.5	43.1	1719	16 US-10-282-122A-39776	Sequence 14455, A
33	1284	43.0	1728	16 US-10-282-122A-14455	Sequence 39295, A
34	1249.5	41.9	1710	15 US-10-369-493-39295	Sequence 39670, A
35	1249.5	41.9	1710	15 US-10-369-493-39670	Sequence 40028, A
36	1249.5	41.9	1710	15 US-10-369-493-40028	Sequence 13519, A
37	1243	41.6	1806	16 US-10-282-122A-13519	Sequence 34030, A
38	1239	41.5	1725	16 US-10-369-493-34030	Sequence 11945, A
39	1222	40.9	1767	16 US-10-282-122A-11945	Sequence 943, App1
40	1166	39.1	1761	15 US-10-156-761-943	Sequence 30639, A
41	1166	39.1	9025608	15 US-10-156-761-1	Sequence 8, App1
42	1101	36.9	1719	16 US-10-282-122A-30639	Sequence 7, App1
43	990.5	33.2	1448	13 US-10-096-571-8	Sequence 3, App1
44	927	31.1	1454	13 US-10-096-571-7	
45	927	31.1	1454	14 US-10-076-416-3	

## ALIGNMENTS

RESULT 1  
US-09-738-626-2873  
; Sequence 2873, Application US/09738626  
; Publication No. US20020197605A1  
GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: MIZOGUCHI, HIROSHI  
; APPLICANT: ANDO, SEIKO  
; APPLICANT: HAYASHI, MIKIRO  
; APPLICANT: OGICHI, KEIKO  
; APPLICANT: YOKOI, HARUHIKO  
; APPLICANT: TATEISHI, NAOKO  
; APPLICANT: SENOH, AKIHIRO  
; APPLICANT: IKEDA, MASATO  
; APPLICANT: OZAKI, AKIO  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; RILE REFERENCE: 249-125  
; CURRENT APPLICATION NUMBER: US/09/738, 626  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: JP 99/377484  
; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: JP 00/159162  
 ; PRIOR FILING DATE: 2000-04-07  
 ; PRIOR APPLICATION NUMBER: JP 00/280988  
 ; PRIOR FILING DATE: 2000-08-03  
 ; NUMBER OF SEQ ID NOS: 7059  
 ; SOFTWARE: Patencin ver. 3.0  
 ; SEQ ID NO: 2873  
 ; LENGTH: 1737  
 ; TYPE: DNA  
 ; ORGANISM: Corynebacterium glutamicum  
 US-09-738-626-2873

Alignment Scores:  
 Pred. No.: 1,71e-272 Length: 1737  
 Score: 2985.00 Matches: 579  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0

US-09-965-825-2 (1-579) x US-09-738-626-2873 (1-1737)

QY 1 MetAlaIserTyrAlaIgluIleuIleAspThrLeuGluAlaGlnGlyValIysArg 20  
 Db 1 ATGGCAGACAGCTACGCGAGACATTAATTGACATTTGAAAGCTCAAGTGTGAAGCGA 60  
 QY 21 IleTyrGlyLeuValGlyAspSerLeuAsnProIleValAspAlaValArgIleSerAsp 40  
 Db 61 ATTTATGCTTTGGTGGGTGACACCTTAATCCGATCTGGAGTCTGCTGCCCAATCAAT 120  
 QY 41 IleGlyThrValHisValArgAsnGluGluAlaAlaIleAspAlaGlyValAspIleSer 60  
 Db 121 ATTGATGGGTGACACCTTGAATAAGAGAGAGCGGCGCTTTGACAGCGCGTGAAGATCG 180  
 QY 61 LeuIleThrGlyGlyLeuValAlaValCysAlaIleSerCysGlyProGlyAsnThrHisIleu 80  
 Db 181 TTGATCAGCTGGGAGAGCTGCGAGATGCTGCTTCTTGTGCTCGGAACACACCTG 240  
 QY 81 IleGlnGlyLeuTyrAspSerHisArgAsnGlyValIysValLeuAlaIleAspHis 100  
 Db 241 ATTCCAGGCTTTAATGATTCGATGAAATGGTGGAAAGTGGTGGCATCGCTAAGCAT 300  
 QY 101 IleProSerAlaGlnIleGlySerThrPheGlnGluThrHisProGluIleLeuPhe 120  
 Db 301 ATTCGAGAGGCCCATTTGGTTCACGTTCTTCCAGAAAGCAGATCCGAGATTTGTTT 360  
 QY 121 LysGluCysSerGlyTyrCysGluMetValAsnGlyIleGlnGlyIleuArgIleLeu 140  
 Db 361 AAGGATGCTCTGCTTACTGCGAGATGGTGAATGGTGGTGAAGCGGTGAACCATTTTG 420  
 QY 141 HisHisAlaIleGlnSerThrMetAlaGlyIleGlyValIleSerValValIleProGly 160  
 Db 421 CATACCGGATTCAGTCCACATGCGGGTAAAGTGTGCGGTGAGTGAATCTTCGTG 480  
 QY 161 AspIleAlaIysGluAspAlaGlyAspGlyThrTyrSerAsnSerThrIleSerSerGly 180  
 Db 481 GATATCCGTAGGAAGACGACGAGTGAAGTACTTAATCCATTCATTTCTTTCTGAC 540  
 QY 181 ThrProValValPheProAspProThrGluAlaAlaAlaLeuValGluAlaIleAsn 200  
 Db 541 ACTCTGTGTGTTCCCGGATCCACTGAGGCTGCGCGCTGTGAGCGCATTAACAC 600  
 QY 201 AlaIysSerValThrLeuPheCysGlyAlaGlyValIleAsnAlaArgAlaGlnValLeu 220  
 Db 601 GCTAAGCTCTGCACTTTGTTCTGCGGCGCGGTAAAGATGCTCGCGCGCATGTTG 660  
 QY 221 GluLeuAlaGluIleValIleYsSerProIleGlyHisAlaLeuGlyGlyIysGlnTyrIle 240  
 Db 661 GAGTTGGCGGAGAAATTAATACCGATCGGGCATGCGCTGGGTGAAGCATACATC 720  
 QY 241 GlnHisGluAsnProPheGluValGlyMetSerGlyLeuLeuGlyTyrGlyValAcVal 260  
 Db 721 CAGCATGAGAAATCGTTTGAAGTGGCATGCTGCGCTGCTTGGTTACGGCGCTGCGTG 780

QY 261 AspAlaSerAsnGluAlaAspLeuLeuIleLeuLeuGlyThrAspPheProTyrSerAsp 280  
 Db 781 GATGCGTCAATGAGGCGGATCTGCTGATTCATTTGGGTACGAGATTTCCCTTATTCGAT 840  
 QY 281 PheLeuProTyrAspAsnValAlaGlnValAspIleAsnGlyValHisIleGlyValArg 300  
 Db 841 TTCCTCTTAAGACACAGCTTGCCAGGTGAGATTCACAGGTGCGACATGTGTGACGT 900  
 QY 301 ThrThrValIleTyrTyrProValThrGlyAspValAlaAlaThrIleGluAsnIleLeuPro 320  
 Db 901 ACCAGGTGAAGTATCCGCTGACCGGTGATGTTGTGCAACATGCAAAATTTTGCTT 960  
 QY 321 HisValIleGluIleThrAspArgSerPheLeuAspArgMetLeuValHisIleGluArg 340  
 Db 961 CATGTGAAGGAAACACAGTCTTCTTCTTGTGATGATGATCTCAAGGACACAGCGGT 1020  
 QY 341 LysLeuSerSerValValGluThrTyrThrHisAsnValGluIleHisValProIleHis 360  
 Db 1021 AAGTTGAGCTCGGTGTGAGAGCTACACACATTAAGTGAAGACATGTGCTTATTC 1080  
 QY 361 ProGlyTyrValAlaSerIleLeuAsnGluLeuAlaAspLysAspAlaValPheThrVal 380  
 Db 1081 CCGAATACGTTCTCTTATTTTGAACAGCTGGCGGATTAAGATGCGGTGTTACTGTG 1140  
 QY 381 AspThrGlyMetCysAsnValThrHisAlaArgTyrIleGluAsnProGluIleThrArg 400  
 Db 1141 GATACCGGATGTGCAATGTGTGATGTGAGTACATCGAGATCCGAGAGAAACGCGC 1200  
 QY 401 AspPheValGlySerPheArgHisGlyThrMetAlaAsnAlaLeuProHisAlaIleGly 420  
 Db 1201 GACTTGTGGTTCATTCGCGCACGCGACGATGGCTAATGTGGTTCGCTCATGCGATTTGT 1260  
 QY 421 AlaGlnSerValAspArgAsnArgGlnValIleAlaMetCysGlyAspArgIleGly 440  
 Db 1261 GCGCAAAAGTGTGATCGAAACCGCGAGGTATCCGATGTGTGCGATGGGTGTTG 1320  
 QY 441 MetLeuLeuGlyGluLeuLeuThrValIleLeuHisGlnLeuProLeuValAlaVal 460  
 Db 1321 ATGCGCTGGGTGACCTTCTAATCGTTAAGCTGACCACTTCGCTGAAGGCGTGGT 1380  
 QY 461 PheAsnAsnSerSerLeuGlyMetValIleLeuGluMetLeuValGluGlnProGlu 480  
 Db 1381 TTATCAACAGTCTTGTGGCATGTGTGAAGTGTGAGATGCTCGTGAAGGACGACGAA 1440  
 QY 481 PheGlyThrAspHisGluGluValAsnPheAlaGluIleAlaAlaIleGlyIleLys 500  
 Db 1441 TTTGATCTGACCATGAGGAATGATTTGCGAGATTTGCGGCGCTGCGGTATCAAA 1500  
 QY 501 SerValArgIleThrAspProLysValArgGluGluLeuAlaGluAlaLeuAlaTyr 520  
 Db 1501 TCGGTACGATACCAACGATCCGAAAGAAATTCGGACAGCTGACCTGACCATTTGGCATAT 1560  
 QY 521 ProGlyProValLeuIleAspIleValThrAspProAsnAlaLeuSerIleProProThr 540  
 Db 1561 CCTGACCTGTACTGATCGATATCGTCAAGSAGCTTAAGCGCTGTGATCCACCAAC 1620  
 QY 541 IleThrTrpGluGluValMetGlyPheSerLysAlaAlaThrArgThrValPheGlyGly 560  
 Db 1621 ATCAGCGGGAACAGGTCAAGGATTCACAGGCGCGCAACCCGAAACGCTTTGTGTGA 1680  
 QY 561 GlyValGlyValaMetIleAspLeuAlaTyrSerAsnIleArgAsnIleProThrPro 579  
 Db 1681 GGAGTGAAGACGATGATGATCTGCGCTTGAACATRAAGAAATATTCATCTCA 1737

# RESULT 2

US-10-781-014-85  
 ; Sequence 85, Application US/10781014  
 ; Publication No. US20040180408A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pompeius, Markus  
 ; APPLICANT: Kroeger, Burkhard  
 ; APPLICANT: Schroder, Hartwig

APPLICANT: Zeider, Oskar  
 APPLICANT: Haberhauser, Gregor  
 TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
 TITLE OF INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY  
 TITLE OF INVENTION: PRODUCTION  
 FILE REFERENCE: BGI-126PCN  
 CURRENT APPLICATION NUMBER: US/10/781.014  
 PRIOR FILING DATE: 2004-02-17  
 PRIOR APPLICATION NUMBER: US 09/602,740  
 PRIOR FILING DATE: 2000-06-23  
 PRIOR APPLICATION NUMBER: 60/141,031  
 PRIOR FILING DATE: 1999-06-25  
 PRIOR APPLICATION NUMBER: 60/143,208  
 PRIOR FILING DATE: 1999-07-09  
 PRIOR APPLICATION NUMBER: 60/151,572  
 PRIOR FILING DATE: 1999-08-31  
 PRIOR APPLICATION NUMBER: DE 19931412.8  
 PRIOR FILING DATE: 1999-07-08  
 PRIOR APPLICATION NUMBER: DE 19931413.6  
 PRIOR FILING DATE: 1999-07-08  
 PRIOR APPLICATION NUMBER: DE 19931419.5  
 PRIOR FILING DATE: 1999-07-08  
 PRIOR APPLICATION NUMBER: DE 19931420.9  
 PRIOR FILING DATE: 1999-07-08  
 PRIOR APPLICATION NUMBER: DE 19931424.1  
 PRIOR FILING DATE: 1999-07-08  
 PRIOR APPLICATION NUMBER: DE 19931428.4  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 784  
 SEQ ID NO 85  
 LENGTH: 1860  
 TYPE: DNA  
 ORGANISM: Corynebacterium glutamicum  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (101)..(1837)  
 OTHER INFORMATION: RXN00635  
 US-10-781-014-85  
 Alignment Scores:  
 Pred. No.: 1,87e-272 Length: 1860  
 Score: 2985.00 Matches: 579  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Gaps: 0  
 DB: 17  
 US-09-965-825-2 (1-579) x US-10-781-014-85 (1-1860)  
 QY 1 MetAlaHisSerTYrAlaGluGluLeuIleAapThrLeuGluValAGlnGlyValIleuArg 20  
 DB 101 ATGGACACACGCTACGCAAGAACAAATTAATGACCTTGGAAAGCTCAAGGTGTGAAGCGA 160  
 QY 21 IleTYrGlyLeuValAGlyAspSerLeuAanProIleValAspAlaValArgGlnSerAsp 40  
 DB 161 ATTTATGTTTGGTGGGTGACAGCCTTAATCGAATCGATGCTGTCTCCGCAATCAGAT 220  
 QY 41 IleGluTrpValHisValArgAsnGluGluAlaAlaAphenAlaAlaGlyValAGlnSer 60  
 DB 221 ATTGAGGTGGTGCACGTTCCGAAATGACGAGACGGCGGCTTGGACGCCGTCGGAATCG 280  
 QY 61 LeuIleThrGlyGluLeuValAlaValAlaSerCysGlyProGlyAanThrHisLeu 80  
 DB 281 TTGATCAGTGGAGACGCTGACGATGATGCTCTTCTTGTGCTCTGGAACACACACCTG 340  
 QY 81 IleGlnGlyLeuTYrAspSerHisArgAsnGlyAlaValValLeuAlaIleAsnSerHis 100  
 DB 341 ATTCAAGGCTCTTATGATTCGACATCGAAATGATGTGGAGAGGTGTGGCATCGCTAGCAT 400  
 QY 101 IleProSerAlaGlnIleGlySerThrPheGlnGluThrHisProGlnIleLeuPhe 120  
 DB 401 ATTCGAGTGCACGATGTTGACGTTCTTCCAGAAACGATCCGAGATTTTGTGT 460

QY 121 LysGluCysSerGlyTYrCysGluMetValAsnGlyGluGlnGlyGluArgIleLeu 140  
 DB 461 AAGGAATGCTCTGGTACTGCGAATGATGTGATGTGTGACAGGCGGAACGATTTTG 520  
 QY 141 HisHsalAlIleGlnSerThrMetAlaGlyGlyGlyValSerValValIleProGly 160  
 DB 521 CATCAGCATTCATGATCCATGCGCGGTAAAGTGTGTGGTGTGATGATTCCTGCT 580  
 QY 161 AspIleAlaValysGluAapAlaGlyAspGlyThrTrpSerAsnSerThrIleSerSerGly 180  
 DB 581 GATATCGCTAAGAAAGACGAGGTACGATCTTAATTCATATTCATATTCCTGCGC 640  
 QY 181 ThrProValValPheProAspProThrGluAlaAlaIleLeuValGluAlaIleAsnAsn 200  
 DB 641 ACTCGTGTGTTCCCGGATCCACTAGAGCTCAGCGCTGCGTGGAGCGCATTTACAC 700  
 QY 201 AlalySerValThrLeuPheCysGlyValAGlyValIleValAsnAlaArgAlaGlnValLeu 220  
 DB 701 GCTAAGTCTGTCACTTGTCTGCGGTCGCGGTGAAGATGCTCCGCGCCAGGTGTG 760  
 QY 221 GluLeuAlaGlyValIleValSerProIleGlyHisAlaLeuGlyGlyValGlyIle 240  
 DB 761 GAGTTGGCGAAGATTAATCAACCATCGGCAATGCGTGGGTGTAGACAGTACATC 820  
 QY 241 GlnHisGluAanProPheGluValAGlyMetSerGlyLeuLeuGlyTYrGlyValACysVal 260  
 DB 821 CAGCATGAGATCCGTTGAGGTGGCATGTCTGGCTGTGTTACGGCGCTGCGGTG 880  
 QY 261 AspAlaSerAsnGluAlaAspLeuLeuIleLeuLeuGlyThrAspPheProTYrSerAsp 280  
 DB 881 GATCGTCCATGAGCGCGATCTGCTGATTCATTTGGGTACGGAATTCCTTATTCAT 940  
 QY 281 PheLeuProValysAspAsnValAlaGlnValAspIleAsnGlyValHisIleGlyValArg 300  
 DB 941 TTCCTCCCTAAGCAACGTTGCCAGGTGATATCAACGTTGGCGCACATTTGTGACGT 1000  
 QY 301 ThrThrValIleTYrProValThrGlyAspValAlaAlaThrIleGluAanIleLeuPro 320  
 DB 1001 ACCACGGTGAAGTATCCGGTACCGGTGATGTTCTGCAACATCGAAATTTTGGCT 1060  
 QY 321 HisValIleGlyGlyValThrAspArgSerPheLeuAspArgMetLeuValHisGluArg 340  
 DB 1061 CATGTGAAGGAAACAAAGATGTTCTCTCTGATGAGATGCTCAAGGACACAGAGGT 1120  
 QY 341 LysLeuSerSerValAGluThrTYrThrHisAsnValAGlyValHisIleValProIleHis 360  
 DB 1121 AAGTTGAGCTCGGTGATGAGACGTACACATTAACGTGAGAGACATGTGCTTATTCAC 1180  
 QY 361 ProGluTYrValAlaSerIleLeuAsnGluLeuAlaAspValAspAlaValPheThrVal 380  
 DB 1181 CTTGATATTCGTTGCTCTTATTTTGAACGAGCTGCGATTAAGATGCGGTTTATCTGTG 1240  
 QY 381 AspThrGlyMetCysAsnValTrpHisAlaArgTYrIleGluAanProGluGlyThrArg 400  
 DB 1241 GATACCGGCAATGTCANATGTGTGCATGCGAGTACATCGAATCCGAGGAGAACGCGC 1300  
 QY 401 AspPheValAGlySerPheValGlyHisIleGlyThrMetAlaAsnAlaLeuProHisAlaIleGly 420  
 DB 1301 GACTTGTGGGTATATTCGCGACGCGACGATGCTTAATGCTGTGCTCATGCAATTTGCT 1360  
 QY 421 AlaGlnSerValAspArgAsnArgGlnValIleAlaMetCysGlyAspGlyGlyLeuGly 440  
 DB 1361 GCGCAAGTGTATTCGAAACCGCAGATGATCCGATGTGTGCGATGTGTGTGGGC 1420  
 QY 441 MetLeuLeuGlyGluLeuLeuThrValIleLeuHisGlnLeuProLeuValAlaVal 460  
 DB 1421 ATGCTGCTGGGTGATCTTGAACGCTTAAGCTGACCAATCTCCGCTGAAGGCTGTGTG 1480  
 QY 461 PheAsnAsnSerSerLeuGlyMetValIleLeuGluMetLeuValAGluGlyGlnProGlu 480  
 DB 1481 TTTAACAACAGTTCTTGTGGCATGTGTGAGATGTCTGCGAGGAGACACACAGAA 1540

Qy 481 PheGlyThrAspHisGluGluValAsnPheAlaGluIleAlaAlaAlaGlyIleAsp 500  
 Db 1541 TTGGTACTGACCATGAGGAGTGAATTTCCAGAGATTTGGGGGGCTGGGGGATCAAA 1600  
 Qy 501 SerValArgIleThrAspProLysValArgGluIleValAlaGluAlaLeuAlaTyr 520  
 Db 1601 TCGGACCAATCACCAGATCCAGAAAGATTCCGAGCGCTGAGGCAATGGCAATAT 1660  
 Qy 521 ProGlyProValIleuIleAspIleValThrAspProAlaLeuSerIleProThr 540  
 Db 1661 CTTGACCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1720  
 Qy 541 IleThrTrpGluGlnValMetGlyPheSerLysAlaAlaThrArgThrValPheGlyGly 560  
 Db 1721 ATCAGTGGAGAACGGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1780  
 Qy 561 GlyValGlyAlaMetIleAspLeuAlaArgSerAsnIleArgAsnIleProThrPro 579  
 Db 1781 GGAAGTGGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1837

## RESULT 3

US-09-965-825-1  
 : Sequence 1, Application US/09965825  
 : Patent No. US20020150999A1  
 : GENERAL INFORMATION:  
 : APPLICANT: THOMAS, Nicole  
 : APPLICANT: THOMAS, Hermann  
 : APPLICANT: THIERRACH, Georg  
 : TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENIC ACID  
 : FILE REFERENCE: 21354USOX  
 : CURRENT APPLICATION NUMBER: US/09/965,825  
 : PRIOR FILING DATE: 2001-10-01  
 : PRIOR APPLICATION NUMBER: DE 10048604.5  
 : PRIOR FILING DATE: 2000-09-30  
 : PRIOR APPLICATION NUMBER: DE 10117085.8  
 : NUMBER OF SEQ ID NOS: 14  
 : SOFTWARE: PatentIn version 3.1  
 : SEQ ID NO 1  
 : LENGTH: 2160  
 : TYPE: DNA  
 : ORGANISM: Corynebacterium glutamicum  
 : FEATURE:  
 : NAME/KEY: CDS  
 : LOCATION: (327)..(2063)  
 : OTHER INFORMATION:  
 : NAME/KEY: -35\_signal  
 : LOCATION: (227)..(232)  
 : OTHER INFORMATION:  
 : NAME/KEY: -10\_signal  
 : LOCATION: (256)..(261)  
 : OTHER INFORMATION:  
 : US-09-965-825-1

## Alignment Scores:

Pred. No.: 2,28e-272 Length: 2160  
 Score: 2985.00 Matches: 579  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Gaps: 0

US-09-965-825-2 (1-579) x US-09-965-825-1 (1-2160)

Qy 1 MetAlaHisSerTyrAlaGluGlnIleuIleAspThrLeuGluAlaGlnGlyValLysArg 20  
 Db 327 ATGGACACAGCTACGCAAGAACATTAATGACCTTGGAGCTCAAGGTGGAAGCGA 386  
 Qy 21 IleTyrGlyLeuValGlyAspSerLeuAsnProIleValAspAlaValAlaArgGlnSerAsp 40  
 Db 387 ATTATAGTTGGTGGGTGACAGCCTTAATCCGATCGTGATGCTGTCCGCCAATCAGAT 446

Qy 41 IleGluTrpValHisValArgAsnGluGluAlaAlaAlaPheAlaAlaGlyIleAsp 60  
 Db 447 ATTGAGTGGGTGACCGTTCGAATGAGGAGCCGGCGCGTTCGACGCCGTGGGATCG 506  
 Qy 61 LeuIleThrGlyGluLeuAlaValCysAlaAlaSerCysGlyProGlyAsnThrHisLeu 80  
 Db 507 TTGATCCTGGGAGGCTGGGAGATGATGCTGCTTCTTGTGGTCCGGAACACACACCTG 566  
 Qy 81 IleGluGlyLeuTyrAspSerHisArgAsnGlyValAluValIleuAlaIleAlaSerHis 100  
 Db 567 ATTCAGGGCTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 626  
 Qy 101 IleProSerAlaGlnIleGlySerThrPhePheGlnGluThrHisProGluIleLeuPhe 120  
 Db 627 ATTCGAGTCCGACGANTGGTTGACCTTCTTCAGGAAGCGATCCGAGATTTTGTGTT 686  
 Qy 121 LysGluCysSerGlyTyrCysGluMetValAsnGlyGlyGluGlnGlyIleuValLeu 140  
 Db 687 AAGGAATGCTCTGTGTTACTGCGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 746  
 Qy 141 HisHisAlaIleGlnIleSerThrMetAlaGlyLysGlyValSerValValIleProGly 160  
 Db 747 CATCAGCGATTCAGTCCACCATGCGCGTAAAGTGTGCGTGTGATGATTCCTGCT 806  
 Qy 161 AspIleAlaLysGluAspAlaGlyAspGlyThrTyrSerAsnSerThrIleSerSerGly 180  
 Db 807 GATATCCCTAAGGAAGACGAGGTGACGATCTTAATCCATTTCCATATTTCTTCTGCG 866  
 Qy 181 ThrProValAlaPheProAspProThrGluAlaAlaAlaLeuValGluAlaIleAsnAsn 200  
 Db 867 ACTCCTGTGTGTTCCCGGATCTTACTGAGGCTGCGCGCTGTGTGAGGCGATTAACAC 926  
 Qy 201 AlaLysSerValThrLeuPheCysGlyAlaGlyValLysAsnAlaArgAlaGlnValLeu 220  
 Db 927 GCTAAGCTGTCACTTGTTCGCGGCGGCTGAAGATCTCGCGCGAGGTG 986  
 Qy 221 GluLeuAlaGluLysIleLysSerProIleGlyHisAlaLeuGlyGlyLysGlnTyrIle 240  
 Db 987 GAGTGGCGGAGGAAGATTAAATCACCGATCGGCAACGCGTGGTGAAGCATTAACATC 1046  
 Qy 241 GlnHisGluAsnProPheGluValGlyMetSerGlyLeuLeuGlyTyrGlyValCysVal 260  
 Db 1047 CACCATGAGATCCGTTTGAGTCCGCGCATGTCGCGCTGCTGTTACCGCGCTCCGCTG 1106  
 Qy 261 AspAlaSerAsnGluAlaAspLeuIleLeuGlyThrAspPheProTyrSerAsp 280  
 Db 1107 GATCGCTCATAGAGCGGATCTGTGATTTTAATGGATACGATTTCCCTTAATCTGAT 1166  
 Qy 281 PheLeuProLysAspAsnValAlaGlnValAspIleAsnGlyValHisIleGlyArgArg 300  
 Db 1167 TTCTTCTTAACACACAGTGGCCAGGTGAGATATCAACGTCGCAATGGTGCACCGT 1226  
 Qy 301 ThrThrValLysTyrProValThrGlyAspValAlaIleThrIleGluAsnIleLeuPro 320  
 Db 1227 ACCACGCTGAGATACCGGTGACCGGTGATGTGTCGCAACATCGAAATATTTGGCT 1286  
 Qy 321 HisValLysGluLysThrAspArgSerPheLeuAspArgMetLeuLysAlaHisGluArg 340  
 Db 1287 CATGTAAAGGAAAAACAGATCGTCTTCTTGAACGAGCTGGCGGATTAAGATCGCTGTTC 1346  
 Qy 341 LysLeuSerSerValAlaGluThrTyrThrHisAsnValGluLysHisValProIleHis 360  
 Db 1347 AAGTTAGCTCGGTGTGAAGAGCTACACACATTAAGTCGAGAGCATGTGCTTAATTC 1406  
 Qy 361 ProGluTyrValAlaSerIleLeuAsnGluLeuAlaAspLysAspAlaValPheThrVal 380  
 Db 1407 CCTGAATACGTGCTCTTAATTTTGAACGAGCTGGCGGATTAAGATCGCTGTTCCTG 1466  
 Qy 381 AspThrGlyMetCysAsnValTyrHisAlaArgTyrIleGluAsnProGluGlyThrArg 400  
 Db 1467 GATACCGGATGTGACATGTGTGCAATGCGAGTATCATGAGAAATCCGAGGAGGAGCC 1526  
 Qy 401 AspPheValGlySerPheArgHisGlyThrMetAlaAsnAlaLeuProHisAlaIleGly 420

Db 1527 GACCTTGGGGTCAATCCGACGACGATGCTAATGGTCCCTCATGCGATTTGCT 1586  
 Qy 421 AAGinservAlaapArgAsnArgGlnValIleAlaMetCysGlyAspGlyVleuGly 440  
 Db 1587 GCGAAAGTGTTCATCCAAACCCGACGGTATTCGGATGTGTGGCGATGTGTGGGC 1646  
 Qy 441 MetLeuenglyGluLeuLeuThrValIleLeuHISGlnLeuProLeuValAlaVal 460  
 Db 1647 ATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTGACCAACTTCGCTGAAAGCTGTGGTG 1706  
 Qy 461 PheAsnAsnSerSerLeuGlyMetValIleLeuGluMetLeuValGluGlyGlnProGlu 480  
 Db 1707 TTTAAACAACAGTTCTTTGGGATGTGTGAAGTTGAAGATGCTGTGGAGGGAACACGAA 1766  
 Qy 481 PheGlyThrAspHisGlnGluValAsnPheAlaGlnIleAlaAlaAlaGlyIleLeu 500  
 Db 1767 TTTGCTACTGACCATGAGAAAGTGAATTTCCAGAGATGGCGGGCTGCGGGATTCMAA 1826  
 Qy 501 SerValArgIleThrAspProIleValAlaArgGlnLeuValAlaValAlaLeuAlaTy 520  
 Db 1827 TCGGTAGGCATCAGCATCCGAAAGAGTTCCGAGACGCTAGCTGAGGCTTTGGCATAT 1886  
 Qy 521 ProGlyProValIleuIleAspIleValIleThrAspProAlaAlaLeuSerIleProThr 540  
 Db 1887 CTGGAACCTGACTGATCATGATATGTCACGATCTTAATGCGTGTGATCCCAACACC 1946  
 Qy 541 IleThrTrpGlnIleValMetGlyPheSerIleAlaIleThrArgThrValPheGlyGly 560  
 Db 1947 ATCCGTGGGAAACGATCATGGATTCAGCAAGCGGCAACCCGAAACCGTCTTGGTGA 2006  
 Qy 561 GlyValGlyAlaMetIleAspLeuAlaArgSerAsnIleArgAsnIleProThrPro 579  
 Db 2007 GGAGTAAAGAGGATGATGATCTGGCCGTTCCAAACATTAAGAAATATTCCTACTCA 2063

RESULT 4  
 US-10-143-856-3  
 ; Sequence 3, Application US/10143856  
 ; Publication No. US20030109014A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BURKE, KEVIN  
 ; APPLICANT: DUNICAN, L.K.  
 ; APPLICANT: MCCORMACK, ASHLING  
 ; APPLICANT: STAPLETON, CLIONA  
 ; APPLICANT: MCKEL, BETTINA  
 ; APPLICANT: THIERBACH, GEORG  
 ; TITLE OF INVENTION: Process for the fermentative preparation of  
 ; TITLE OF INVENTION: with amplification of the tkt gene  
 ; FILE REFERENCE: MAS/021123/282432  
 ; CURRENT FILING DATE: 2002-05-14  
 ; PRIOR APPLICATION NUMBER: US/10/143,856  
 ; PRIOR FILING DATE: 17-03-2000  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 2160  
 ; TYPE: DNA  
 ; ORGANISM: Corynebacterium glutamicum  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (327)..(2063)  
 ; OTHER INFORMATION: poxb  
 US-10-143-856-3

Alignment Scores:  
 Pred. No.: 2,28e-272 Length: 2160  
 Score: 2985.00 Matches: 579  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 15 Gaps: 0

US-09-965-825-2 (1-579) x US-10-143-856-3 (1-2160)  
 Qy 1 MetAlaHisSerIleValAlaGlnLeuIleAspThrLeuGluAlaGlnGlyValIleArg 20  
 Db 327 ATGGCAACACACCTACCGAAGAACATTAATTACACTTTGAAAGCTCAAGAGGTGAAGCA 386  
 Qy 21 IleTyGlyLeuValGlyAspSerLeuAsnProIleValAspAlaValArgGlnSerAsp 40  
 Db 387 ATTTATGTTTGGGTGAGGAGCAAGCTTAATCCGATCGTGAATGCTGCCCAATTCAGAT 446  
 Qy 41 IleGluTrpValHisValArgAsnGlnGluAlaAlaPheAlaAlaGlyValAlaGlnSer 60  
 Db 447 ATTAGAGGGGTGACGTTCCAAAGAGAAAGCGGCGGCTTTGACGCGGTGGCAATTCG 506  
 Qy 61 LeuIleThrGlyGluLeuAlaValCysAlaAlaSerCysGlyProGlyAsnThrHisIleu 80  
 Db 507 TTGATCACTGGGAGGCTGGCGATATGCTGCTTTCTTGTGCTCTGAAACACACACTTG 566  
 Qy 81 IleGlnGlyLeuTyraAspSerHisArgAsnGlyAlaIleValLeuAlaIleAlaSerHis 100  
 Db 567 ATTCAGGGGTCTTATGATTCGATCGAAATGTCGAAGGTGTGGCATGCTAGCAT 626  
 Qy 101 IleProSerAlaGlnIleGlySerThrPhePheGlnGluThrHisProGluIleLeuPhe 120  
 Db 627 ATTCGAGTGGCCGATTTGGTTCGACGCTCTTCCAGGAACGCAATCCGAGATTTGTTT 686  
 Qy 121 LysGluCysSerGlyTyraCysGluMetValAsnGlyGlyGlnGlnGlyValArgIleLeu 140  
 Db 687 AAGGAATGCTCTGTGATCTGAGATGTGAATGTGTGTGAAGCGGGTGAACGCAATTTG 746  
 Qy 141 HisHisAlaIleGlnSerThrMetAlaGlyValSerGlyValSerValAlaIleProGly 160  
 Db 747 CATCAGCGCATTCAGTCCACATGCGGGTAAAGTGTGTGCGGTAGATTCCTGGT 806  
 Qy 161 AspIleAlaIleGlyAspAlaGlyAspGlyThrTyraSerAsnSerThrIleSerSerGly 180  
 Db 807 GATATTCCTAAGGAAGACGACGATGACGATTAATTCATTCATTAATTCCTTCTGCGC 866  
 Qy 181 ThrProValAlaPheProAspProThrGluAlaAlaIleuValGluAlaIleAsnAsn 200  
 Db 867 ACTCTGTGTGTGTCGGAATCTTACTGAGGCTGACGCTGGTGGGCGGATTAACAC 926  
 Qy 201 AlaIleSerValThrLeuPheCysGlyAlaGlyValAlaIleAsnAlaArgAlaGlnValLeu 220  
 Db 927 GCTAAGTCTGACTTTGTTCTGCGGTGGCGGCTGAAGATGCTCCGCGCAGGTGTTG 986  
 Qy 221 GluLeuAlaGluValIleIleSerProIleGlyHisAlaLeuGlyGlyIleGlnTyrlle 240  
 Db 987 GAGTTGGCGGAGAAGATTAAATACACGATCGGGCATGCGTGGGTGTAAGCAGTACATC 1046  
 Qy 241 GlnHisGluAsnProPheGluValGlyMetSerGlyLeuLeuGlyTyrlGlyAlaCysVal 260  
 Db 1047 CAGATAGAAATCCGTTGAAGTCGCGCATGTGCGCTGTGTTAGCGCGCTGGGTG 1106  
 Qy 261 AspAlaSerAsnGluAlaAspLeuLeuIleLeuGlyThrAspPheProTyraSerAsp 280  
 Db 1107 GATCGCTCAATGAGGCGGATCTGCTGATCTTAATGGGTACGATTTCCCTTATTCGAT 1166  
 Qy 281 PheLeuProIleAspAsnValAlaGlnValAspIleAsnGlyAlaHisIleGlyArgArg 300  
 Db 1167 TTCCTTCTTAAGCAACAGTTCGCGCAGGTGATATCAACGTGGGCAATGTGGTCAAGT 1226  
 Qy 301 ThrThrValIleTyraProValThrGlyAspValAlaAlaThrIleGluAsnIleLeuPro 320  
 Db 1227 ACCACGCTGAAGATTCGCTGACCGGTGATGTGCTGCAACATCGAAATATTTTGGCT 1286  
 Qy 321 HisValIleGlyIleTyraAspSerPheLeuAspArgMetLeuTyraHisGlyArg 340  
 Db 1287 CATGTGAAGAAACAAACAGTCTTCTTCTGATGATGCTCAAGGACACAGAGCT 1346  
 Qy 341 LysLeuSerSerValAlaGluThrTyraHisAsnValGluTyraHisValProIleHis 360  
 Db 1347 AAGTTAGCTCGGTGTGAAGACGTACACATTAAGTCAAGAAAGCATGTGCTTATTCAC 1406

QY	361	ProGluTyrValAlaSerIleLeuAsnGluLeuAlaAspIysAspAlaValPheThrVal	380
DB	1407	CTGGAATACGCTGCTTATTTTGAACGAGCTGGCGATGAAGATGGGCTTTACTGTG	1466
QY	381	AspThrGlyMetCysAsnValTrpHisAlaArgTyrIleGluAsnProGluGlyThrArg	400
DB	1467	GATACCGGATGTCATATGTGTGTCATGCGAGTACATCCGAAATCCGAGGGAAACCGCG	1526
QY	401	AspPheValGlySerPheArgHisGlyThrMetAlaAsnAlaLeuProHisAlaIleGly	420
DB	1527	GACTTGTGGGTTCATTCGCGACAGGACCATGGCTATATGCTTGCCTCATGCGATTGT	1586
QY	421	AlaGlnSerValAspArgAsnArgGluValIleAlaMetCysGlyAspGlyGlyLeuGly	440
DB	1587	GCGGAAGTGTGATTCGAACCCGCAAGTGAATCCGATGCTGCGCATGGGTGTGGGC	1646
QY	441	MetLeuLeuGlyGluLeuLeuThrValIlyLeuHisGlnLeuProLeuValAlaVal	460
DB	1647	ATGCTGCTGGGTGATTCGACCGTTAAGCTGCACCACTTCCGCTGAAGGCTGTGTG	1706
QY	461	PheAsnAsnSerSerLeuGlyMetValIlyLeuGluMetLeuValGluGlyGlnProGlu	480
DB	1707	TTTAAACAACAGTTCTTTGGGATGTGAAGTTGAGATGCTGCTGGAGGACACCGCAA	1766
QY	481	PheGlyThrAspHisGluGluValAsnPheAlaGluIleAlaIleAlaGlyIleLys	500
DB	1767	TTTGTCTACATCCATGAGGAAGTGAATTTCCGACAGATTCGCGCGCTCCGCGTACAA	1826
QY	501	SerValArgIleThrAspProLysValArgGluGlnLeuAlaGluAlaLeuAlaTyr	520
DB	1827	TCGGTAGCATACCGATCCGAAGAAAGTTGCGAGACGCTAGCTGAGGACATTGGCATAT	1886
QY	521	ProGlyProValLeuIleAspIleValThrAspProAsnAlaLeuSerIleProProThr	540
DB	1887	CTGGACCTGACTGATCGATCGATCTGACGATCTTAATGGCTGATGCCACCAACC	1946
QY	541	IleThrTrpGluGlnValMetGlyPheSerIysAlaIleThrArgThrValPheGlyGly	560
DB	1947	ATCACGGGGAACAGTCAATGGATTTCAGCAAGCGCGCCACCCGACCGCTTTGGTGA	2006
QY	561	GlyValGlyAlaMetIleAspLeuAlaArgSerAsnIleArgAsnIleProThrPro	579
DB	2007	GGAGTAGAGAGATGATCGATCTGGCCGTTCCGAACATTAAGATATTTCTACTCCA	2063
RESULT 5			
US-10-078-167-4			
; Sequence 4, Application US/10078167			
; Publication No. US20030119154A1			
; GENERAL INFORMATION:			
; APPLICANT: Dunican, Rita			
; APPLICANT: McCormack, Ahling			
; APPLICANT: Stapleton, Cliona			
; APPLICANT: Burke, Kevin			
; APPLICANT: Mockel, Bettina			
; TITLE OF INVENTION: Process for the preparation of L-amino acids using			
; FILE REFERENCE: 990229 BR-US-B			
; CURRENT APPLICATION NUMBER: US/10/078,167			
; NUMBER OF SEQ ID NOS: 16			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 4			
; LENGTH: 2160			
; TYPE: DNA			
; ORGANISM: Corynebacterium glutamicum			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (327)..(2063)			
; OTHER INFORMATION: poxb			
US-10-078-167-4			
Alignment Scores:			

Pred. No.:	2,28e-272	Length:	2160
Score:	2985.00	Matches:	579
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	15	Gaps:	0

US-09-965-825-2 (1-579) x US-10-078-167-4 (1-2160)

QY	1	MetAlaHisSerTyrAlaGluGlnLeuIleAspThrLeuGluAlaGlnGlyValLysArg	20
DB	327	ATGGCACACGCTTACCGCAACATTAATTATTAACCTTTGGAAGCTCAAGGTGTGAACCGA	386
QY	21	IleTyrGlyLeuValGlyAspSerLeuAsnProIleValAspAlaValArgGlnSerAsp	40
DB	387	ATTATATGTTTGGTGGGTGACACCTTAATCCATGTGTGATGCTGTCCGCAATGAT	446
QY	41	IleGluTrpValHisValArgAsnGluGluAlaAlaPheAlaAlaGlyValAlaGlnSer	60
DB	447	ATTGAGTGGGTGACCTTCGAATGAAGAACCGCGCTTTCAGCCGCTGGGATTCG	506
QY	61	LeuIleThrGlyGluLeuAlaValCysAlaAlaSerCysGlyProGluAsnThrHisLeu	80
DB	507	TTATATCATGGGAGAGCTGGGAGATATGCTGCTTTGTGTGCTGGAAACACACCTTG	566
QY	81	IleGlnGlyLeuTyrAspSerHisArgAsnGlyValAlaValLeuAlaIleAsnHis	100
DB	567	ATTCAAGGCTTTTATATATTCGATTCGAATGATGCGAAGGTGTGGCATCGCTAGCAT	626
QY	101	IleProSerAlaGlnIleGlySerThrPhePheGlnGluThrHisProGluIleLeuPhe	120
DB	627	ATTCCAGTGTCCAGATGTGGTTCAGAGTCTTCCAGGAACCGATCCGAGATTTGT	686
QY	121	LysGluCysSerGlyTyrCysGluMetValAsnGlyGlyGluGlnGlyLysArgIleLeu	140
DB	687	AAGAAATGCTTGATCTGATCTGCGAATGTGAATGGTGTGAACAAGGTGAACGATTTTG	746
QY	141	HisHisAlaIleGlnSerThrMetAlaGlyLysGlyValSerValValIleProGly	160
DB	747	CATCAGCGCATTCAGTCCACCATGGCGGTAAAGGTGTGCGGTGATGATTCCTGGT	806
QY	161	AspIleAlaLysGluAspAlaGlyAspGlyThrTyrSerAsnSerThrIleSerSerGly	180
DB	807	GATATCGCTTAAGAAAGACGCGAGTGAACGTAATTCATTCCTAATTCCTATTTCTTGGC	866
QY	181	ThrProValValPheProAspProThrGluAlaAlaLeuValGluAlaIleAsnAsn	200
DB	867	ACTCTGTGTGTTCCTCGATCTTACTGAGGCTGACGCTGGTGAAGCGATTAACAC	926
QY	201	AlaLysSerValThrLeuPheCysGlyAlaGlyValLysAsnAlaArgAlaGlnValLeu	220
DB	927	GCTAAGCTGTCACTTTGTTCTCGCGGGGGGTGAAGAAATCTCGCGGACAGGTGTG	986
QY	221	GluLeuAlaGluLysIleLysSerProIleGlyHisAlaLeuGlyGlyLysGlnTyrIle	240
DB	987	GAGTTGGCGGAAGAATTAAATCAACGATCGGCAATCGCTGGGTGTGAAGCATATC	1046
QY	241	GlnHisGluAsnProPheGluValGlyMetSerGlyLeuLeuGlyTyrGlyAlaCysVal	260
DB	1047	CAGCATGAAGATCCGTTGAGTGGCATGTGCGCTGTGTTTGATTCGCGCTGCGTG	1106
QY	261	AspAlaSerAsnGluAlaAspLeuLeuIleLeuGlyThrAspPheProTyrSerAsp	280
DB	1107	GATCGCTCCATGAGGGGATTCGCTGATTCATTTGGGTATCGGATTTCCCTTATTCGAT	1166
QY	281	PheLeuProLysAspAsnValAlaGlnValAspIleAsnGlyAlaHisIleGlyAlaArg	300
DB	1167	TTCTTCTTAAGACAACGTTGCCAGGTGATATCAACGTCGCGACATATGTGTGCGCT	1226
QY	301	ThrThrValLysTyrProValThrGlyAspValAlaAlaThrIleGluAsnIleLeuPro	320
DB	1227	ACCACGCTGAAGTATCGGTGACCGGATGATGTGTCGAACATCGAAATATTTTGCT	1286







QY 281 PheLeuProLYAspAsnValAlaGlnValAspIleAsnGlyAlaHisIleGlyArgArg 300  
 Db 1167 TTCCTTCTTAAGCAACGTTGCCAGGTGGATATCAACGGTGGCAATGTTGGACCT 1226  
 QY 301 ThrThrValIleYrProValIleThrGlyAspValAlaAlaThrIleGluAsnIleLeuPro 320  
 Db 1227 ACCACGGGAGAGTATCCGGTACCGGTGATGTTGTGCACAAATCAATCAAAATATTTGGCT 1286  
 QY 321 HisValIleGlyIleThrAspArgSerPheLeuAspArgMetLeuValAlaHisIleGluArg 340  
 Db 1287 CATGTGAAGGAAAAACAGATCGTCTCTTCTTGTATCGAATGCTTCAGGCAACAGAGCGT 1346  
 QY 341 LysLeuSerSerValIleGlnThrTyrThrHisAsnValGluYrHisValProIleHis 360  
 Db 1347 AAGTTGAGCTCGGTGTGAGACGTACACATACATACGTGAGAAAGCATGTCCTATTCAC 1406  
 QY 361 ProGluYrValAlaIleSerIleLeuAsnGluLeuAlaAspIleAspAlaValPheThrVal 380  
 Db 1407 CCTGAATACGTTGCTCTATTTTGAACGACGTGGCGGATAGGATGGGTTTATCTGTG 1466  
 QY 381 AspThrGlyMetCysAsnValTyrHisAlaArgTyrIleGluAsnProGluGlyThrArg 400  
 Db 1467 GATACCGGATGTCATGTCATGTCGCAATCCGAGTACATCCAGATCCGAGGCAACGGCC 1526  
 QY 401 AspPheValGlySerPheArgHisIleGlyThrMetAlaAsnAlaLeuProHisAlaIleGly 420  
 Db 1527 GACTTGTGGGTTCATTCGCCGACGCAACGATAGCTATATGCTTATGCTCATGCGATTCGT 1586  
 QY 421 AlaGlnSerValAspArgAsnArgGlnValIleAlaMetCysGlyIleAspGlyIleGly 440  
 Db 1587 GCGCAAGTGTGATCCAAACCGCCAGGTGATCCGAGTGTGGCGATGGTGTGTGTGGCC 1646  
 QY 441 MetLeuLeuGlyIleLeuLeuThrValIleLeuHisIleGlnLeuProLeuValAlaVal 460  
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 QY 461 PheAsnAsnSerSerLeuGlyMetValIleLeuGluMetLeuValGluGlyIleProGlu 480  
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 QY 481 PheGlyThrAspHisGluGlnValAsnPheAlaGluIleAlaAlaAlaGlyIleLeu 500  
 Db 1767 TTTGATCTGACATGAGAGTCAATTTTCGACAGATGCGGGGCTGGCGGTATCAA 1826  
 QY 501 SerValArgIleThrAspProLYIleValAlaArgGluIleuAlaGluAlaLeuAlaTyr 520  
 Db 1827 TCGGTACGATCAACGATCCGAGAAAGTTCCGAGACAGCTAGCTAGGCAATTCAT 1886  
 QY 521 ProGlyProValIleuIleAspIleValIleThrAspProAsnAlaLeuSerIleProThr 540  
 Db 1887 CTTGGAACCTTACTGATCGATATGTCACGATCTCTATGCGCTGTGATCCACCAACC 1946  
 QY 541 IleThrTyrGluGlnValMetGlyPheSerIleAlaIleThrArgThrValPheGlyIle 560  
 Db 1947 ATACCGTGAACAGGTACGATCGGATTCAGCAAGCGGCCAACCGGACCTTTGGTGA 2006  
 QY 561 GlyValGlyAlaMetIleAspLeuAlaArgSerAsnIleArgAsnIleProThrPro 579  
 Db 2007 GGAGTAGAGACGATGATCGATCGGCCGTTCCGAAACATTAATATCTCACTCCA 2063  
 RESULT 7  
 US-10-091-342-4  
 ; Sequence 4, Application US/10091342  
 ; Publication No. US20030199045A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Degussa AG  
 ; APPLICANT: National University of Ireland, Galway  
 ; APPLICANT: Forschungszentrum Juilich GmbH  
 ; TITLE OF INVENTION: Process for the fermentative Preparation of L-Amino Acids with  
 ; TITLE OF INVENTION: Amplification of the zwf Gene.  
 ; FILE REFERENCE: 990239BT  
 ; CURRENT APPLICATION NUMBER: US/10/091,342  
 ; CURRENT FILING DATE: 2002-03-06

; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 4  
 ; LENGTH: 2160  
 ; TYPE: DNA  
 ; ORGANISM: Corynebacterium glutamicum  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (327)..(2063)  
 ; OTHER INFORMATION: poxb  
 US-10-091-342-4  
 Alignment Scores:  
 Pred. No.: 2,28e-272 Length: 2160  
 Score: 2985.00 Matches: 579  
 Percent Similarity: 100.008 Conservative: 0  
 Best Local Similarity: 100.004 Mismatches: 0  
 Query Match: 100.004 Indels: 0  
 DB: 15 Gaps: 0  
 US-09-965-825-2 (1-579) x US-10-091-342-4 (1-2160)  
 QY 1 MetAlaHisSerTyrAlaGlnGlnLeuIleAspThrLeuGlnAlaGlnGlyValIleYrArg 20  
 Db 327 ATGGCAACACGATACGCAAGAAACATTAATTGACACTTGGAACTCAAGGTGTGAAGCA 386  
 QY 21 IleTyrGlyLeuValGlyAspSerLeuAsnProIleValAspAlaValAlaArgIleSerAsp 40  
 Db 387 ATTATAGTGTGTGTGGGTGACAGCTTAAATCCATGCTGATCTGTCCGCAATCAGAT 446  
 QY 41 IleGlnTyrValHisValArgAsnGluGlnAlaAlaAlaPheAlaAlaGlyAlaGluSer 60  
 Db 447 ATTAGAGGTGTGACGTTGCAATGAGAAAGCGCGGCTTTCACCGGTGCGAATCG 506  
 QY 61 LeuIleThrGlyIleLeuAlaValCysAlaAlaSerCysGlyProGlyAsnThrHisLeu 80  
 Db 507 TTATATCATCGGGAGGTGGCGATGATGCTGCTTCTGTGTGCTCGAAACACACACCTG 566  
 QY 81 IleGlnGlyLeuTyrAspSerHisArgAsnGluValAlaValIleuAlaIleAlaSerHis 100  
 Db 567 ATTCAGGGTCTTATATATTCGATCAATGAGCAAGGTGTGGCAATGCTTACGCCAT 626  
 QY 101 IleProSerAlaGlnIleGlySerThrPhePheGlnGluThrHisAspProGluIleLeuPhe 120  
 Db 627 ATTCGAGTGGCCCAAGATTGGTTCGACGTTCTTCAGAAACGATCCGAGATTTGTT 686  
 QY 121 LysGluCysSerGlyTyrCysGluMetValAsnGlyGlyGluGlnGlyIleuArgIleLeu 140  
 Db 687 AAGGAATGCTCTGTACTGCGAGATGCGATGATGTTGTGTGAGCAGCGGTGAACGCATTTTG 746  
 QY 141 HisHisAlaIleGlnSerThrMetAlaGlyIleValSerValValIleProGly 160  
 Db 747 CATACGCCATTCAGTCCACCATGCGGGTAAAGTGTGTGCGGTGATGATTCCTGCT 806  
 QY 161 AspIleAlaLysGluAspAlaGlyAspGlyThrTyrSerAsnSerThrIleSerSerGly 180  
 Db 807 GATATCGCTAAGGAAGACCAAGGTGACGATATTAATCAATTCACATATTTCTTCTGCG 866  
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 Db 927 GCTAAGTCTGTCACTTTGTTCTGCGGTGCGGCGTGAAGAAAGCTCGCGCGAGGTGTG 986  
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 Db 987 GAGTTGGCGGAAGATTAATCAACGATCGGCAATGCGCTGGGTGTGAAGCATATC 1046  
 QY 241 GlnHisGluAsnProPheGluValGlyMetSerGlyLeuLeuGlyTyrGlyAlaCysVal 260  
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QY 281 PheLeuProGlyAspAsnValAlaGlnValAspIleAsnGlyAlaHisIleGlyArg 300
DB 1167 TTCTTCTTAAGACCAAGTTCGACAGTGAATACAGGTGGACCATTTGGTCAGCGT 1226
QY 301 ThrThrValIleTyrProValThrGlyAspValAlaAlaThrIleGluAsnIleLeuPro 320
DB 1227 ACCACGGTGAAGTATCCGGTACCGGTGATGTTCTTCAACATCGAAATATTTTCCCT 1286
QY 321 HisValIleGlyLeuThrAspArgSerPheLeuAspArgMetLeuValAlaHisIleGlyArg 340
DB 1287 CATGTGAAGGAAAAACAGATCGTTCTTCTTGAATCGGATGTCAGAGGACAGACGCGT 1346
QY 341 LysLeuSerSerValValIleGlyThrThrHisAsnValAlaGlyValIleValProIleHis 360
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QY 361 ProGlyTyrValAlaSerIleLeuAsnGluLeuAlaAspLysAspAlaValPheThrVal 380
DB 1407 CCGTAATACGTTGCTTATTTTGAACGAGCTGGCGGATTAAGATGCGGTGTTTACTGTG 1466
QY 381 AspThrGlyMetCysAsnValIlePheAlaArgTyrIleGluAsnProGlyIleThrArg 400
DB 1467 GATACCGGATGTCATGTGTGCGATGTGCGATGCGAGATGCGATGCGAGGAGGAGCGC 1526
QY 401 AspPheValIleGlySerPheArgHisIleGlyThrMetAlaAsnAlaLeuProHisAlaIleGly 420
DB 1527 GACTTGTGGGTTCATTCCTCCGACGCGACATGCTTATGCTTCCCTCAGTCATGCTGT 1586
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QY 481 PheGlyThrAspHisIleGlyIleValAsnPheAlaGluIleAlaAlaAlaGlyIleLys 500
DB 1767 TTGTGTACTGACATGAGAGGAAATTCGAGAGATTCGCGCGCTGCGGTATCAA 1826
QY 501 SerValArgIleThrAspProLysLysValArgGluIleLeuAlaLeuAlaTyr 520
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QY 521 ProGlyProValIleLeuIleAspIleValThrAspProAsnAlaLeuSerIleProProThr 540
DB 1887 CCGGACCTGTATCGATCGATTCGATCGGATTCCTTAATGCGGTGATCCCAACACC 1946
QY 541 IleThrTyrGluGlnValMetGlyPheSerLysAlaAlaThrArgThrValPheGlyIle 560
DB 1947 ATCACTGGGACAGGTCATGAGATTCAGACAGCGCGCACCGCAACCGCTTTGGTGGGA 2006
QY 561 GlnValAlaValMetIleAspLeuAlaArgSerAsnIleArgAsnIleProThrPro 579
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; Sequence 4, Application US/10686736
; Publication No. US20040063181A1
; GENERAL INFORMATION:
; APPLICANT: Dunican, Rita
; APPLICANT: McCormack, Ashling
; APPLICANT: Stapleton, Cliona

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; APPLICANT: Burke, Kevin
; APPLICANT: Mookel, Bettina
; TITLE OR INVENTION: Process for the preparation of L-amino acids using
; FILE REFERENCE: 990229 BT-US-B
; CURRENT APPLICATION NUMBER: US/10/686,736
; PRIOR FILING DATE: 2003-10-17
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentia Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2160
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (327)..(2063)
; OTHER INFORMATION: poxb
US-10-686-736-4

Alignment Scores:
Pred. No.: 2,28e-272 Length: 2160
Score: 2985.00 Matches: 579
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-09-965-825-2 (1-579) x US-10-686-736-4 (1-2160)
QY 1 MetAlaHisSerTyrAlaGluGlnLeuIleAspThrLeuGluAlaGlnGlyValLysArg 20
DB 327 ATGGACACAGCTACGAGAGAACATTAATTAATGACACTTGAAGTCAAGGTGAGACGA 386
QY 21 IleTyrGlyLeuValGlyAspSerLeuAsnProIleValAspAlaValAlaArgIleSerAsp 40
DB 387 ATTATAGTTGGTGGGTGATGACCTTAATCCGATCGTGAATCGTGTCCGCCAATCAT 446
QY 41 IleGluThrValHisValArgAsnGluGlnAlaAlaPheAlaAlaGlyAlaGlyIle 60
DB 447 ATTAGAGGTGTGACGTTTCAAAATGAGAGAGCGCGGCTTTGCGAGCGGTGCGAAATCG 506
QY 61 LeuIleThrGlyIleLeuAlaValCysAlaAlaSerCysGlyProGlyAsnThrIleLeu 80
DB 507 TTATACCTGGGAGCTGGAGATGTGTGCTTCTTGTGTGCTTGTGAAACACACACTTG 566
QY 81 IleGlnGlyLeuTyrAspSerHisArgAsnGlyValAlaValLeuAlaIleAsnHis 100
DB 567 ATTCAGGCTTTATGATTCGATTCGAATGAGCGAAGGTGTGGCATCGCTAGCCAT 626
QY 101 IleProSerAlaGlnIleGlySerThrPhePheGlnGluThrHisProGluIleLeuPhe 120
DB 627 ATTCGAGTCCCAAGATTTGTTGACGTTCTTCAGAGAAACGATCCGAGATTTGTTT 686
QY 121 LysGluCysSerGlyTyrCysGluMetValAsnGlyIleGluGlnGlyIleArgIleLeu 140
DB 687 AAGGAATGCTCTGTATCTGAGATGTGAAGGTGTGAAGGAGGAGGAGGAGGAGGAGGAG 746
QY 141 HisHisAlaIleGlnSerThrMetAlaGlyLysGlyValSerValValIleProGly 160
DB 747 CATCACCGCATTAAGTCCACCATGCGCGGTAAAGTGTGTGCGGTGAAGATTCCTGCT 806
QY 161 AspIleAlaLysGluAspAlaGlyAspGlyThrTyrSerAsnSerThrIleSerSerGly 180
DB 807 GATATCGCTAAGAAACAGCAGGTGACGATCTTAATTCCTAATTCCTAATTCCTTCCG 866
QY 181 ThrProValValPheProAspProThrGluAlaAlaLeuValGluAlaIleAsnAsn 200
DB 867 ACTCTGTGTGTTCCTCCGATCTTACTAGAGGTGACAGCGTGTGTGAAGGAGATTAACAC 926
QY 201 AlaLysSerValThrLeuPheCysGlyAlaGlyValIleAsnAlaArgAlaGlnValLeu 220

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Db 927 GCTAAGTCGTCACTTTGTCGCGGTGCGGCGGTGAAGATGCTGCGCGCGAGGTGTTG 986  
 QY 221 GlnLeuAlaGluIysIleYsSerProIleGIYHISAlaLeuGIYLYSGINTRYIle 240  
 Db 987 GAGTTGGCGGAGAAATTAATCAACCATCGGCATCGCTGGGTGGTAAAGCATATC 1046  
 QY 241 GlnHISGluAnDProPheGluValaGlyMetSerGIYLeuLeuGIYTRYGlyAlaCysVal 260  
 Db 1047 CACACATGAGATCCGTTTGAGGTGCGCATGTCGCTGCTGGTATTAACGCGCTGCGTG 1106  
 QY 261 AspAlaSerSerndGluAlaLeuLeuIleLeuLeuGIYThrAspPheProYrSerAsp 280  
 Db 1107 GATGCGCATATAGGCGGATCGCTGATTCATATGGGTACGGAATTCCTTATTCGAT 1166  
 QY 281 PheLeuProIysAspSerValaAlaGlnValaAspIleAnGIYAlaHISileGIYArg 300  
 Db 1167 TTCCTTCCTTAACACACGTTGGCCAGGTGATATCAACGTCGCGCATTTGGTCAAGCT 1226  
 QY 301 ThrThrValIysTYrProValIThrGIYAspValaAlaAlaThrIleGluAnIleLeuPro 320  
 Db 1227 ACCACGGTGAAGTATCGGTGACCGGTGATGTTGCTCAACATCGAAATATTTGGCT 1286  
 QY 321 HisValIleGluIysThrAspArgSerPheLeuAspArgMetLeuIysAlaHISGluArg 340  
 Db 1287 CATGTAAAGGAAAAACAGATCGTTCCTTCCTTGATCGAATGCTCAAGCACACGACCGCT 1346  
 QY 341 LysLeuSerSerValaGluThrTYrThrHISAsnValaGluIysHISValaProIleHIS 360  
 Db 1347 AAGTTAGCTCGGTGGTAGACGTACACATACATCGTCAAGAAACATGTCCTTATTCAC 1406  
 QY 361 ProGluTYrValaAlaSerIleLeuAnGluLeuAlaAspIysAspAlaValaPheThrVal 380  
 Db 1407 CCGTAATAGCTGCTCTATTTTGAACGAGCTGGCGGATAGAGATGGGGTTTACGTG 1466  
 QY 381 AspThrGIYMetCysAsnValITPPhISAlaArgTYrIleGluAnProGIYUGLYThrArg 400  
 Db 1467 GATACCGGCGATGTCATGTGTGACATGTCAGAGTACATCAAGATCCGAGGGAGCGCGC 1526  
 QY 401 AspPheValaGlySerPheArgHISGIYThrMetAlaAsnAlaLeuProHISAlaIleGIY 420  
 Db 1527 GACTTTGTGGTTCATTCGCCACGCGACGATGGCTATATCGCTTGCCTCATCGCATTTG 1586  
 QY 421 AlaGlnSerValaAspArgAsnArgIValaIleAlaMetCysGIYAspGIYLYLeuGIY 440  
 Db 1587 GCGCAAGTGTATGAAACCCGACGATGATCGCATGTGCGCATGTGTTGGGCG 1646  
 QY 441 MetLeuLeuGIYGIYLeuLeuThrValaIysLeuHISGluLeuProIleIysAlaVala 460  
 Db 1647 ATGCTGCTGGGTGAGCTTCTGACCGGTAAAGCTCACCAACTTCGCTGAAGGCTGTGGTG 1706  
 QY 461 PheAsnAsnSerSerLeuGIYMetValaIysLeuGIYMetLeuValaGluGIYInProGIY 480  
 Db 1707 TTTTAAACAAGTCTTTGGGACATGTGAATTTGAGATGCTCGTGGAGGACAGCGA 1766  
 QY 481 PheGIYThrAspHISGluGluValaAsnPheAlaGluIleAlaAlaAlaGIYIleYs 500  
 Db 1767 TTTTGATACGACATAGAGAAAGATTTTCGACAGATTTGCGCGCGCTGGGTATCAAA 1826  
 QY 501 SerValaArgIleThrAspProIysIysValaArgGluGluLeuAlaGluAlaLeuAlaTYr 520  
 Db 1827 TCGGTACGATCACCATCGAAGAAAGTTCCGACAGACGTAAGCATGGCATTTGGCATAT 1886  
 QY 521 ProGluProValaLeuIleAspIleValaThrAspProAsnAlaLeuSerIleProProThr 540  
 Db 1887 CCGGACCTGATATCATATCATATCATATCATATCATATCATATCATATCATATCATAT 1946  
 QY 541 IleThrTrpGluGluValaMetGIYPheserIysAlaAlaThrArgThrValaPheGIY 560  
 Db 1947 ATCAAGTGGGAACAGATCATGGATTCAGCAAGCGCGCACCCGAAACGCTTTGGTGA 2006  
 QY 561 GLYValaGlyAlaMetIleAspLeuAlaArgSerAsnIleArgAsnIleProThrPro 579  
 Db 2007 GGAGTGGAGGAGATGATCATGTGCGCCGTTGGAACATTAAGAAATATTCCTACTCA 2063

RESULT 9  
 US-09-965-825-4  
 ; Sequence 4, Application US/09965825  
 ; Patent No. US20020150999A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DUSCH, Nicole  
 ; APPLICANT: THOMAS, Hermann  
 ; APPLICANT: THIERBACH, Georg  
 ; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENOIC ACID US  
 ; TITLE OF INVENTION: CORYNEFORM BACTERIA  
 ; FILE REFERENCE: 21354USOX  
 ; CURRENT APPLICATION NUMBER: US/09/965, 825  
 ; CURRENT FILING DATE: 2001-10-01  
 ; PRIOR APPLICATION NUMBER: DE 10048604.5  
 ; PRIOR FILING DATE: 2000-09-30  
 ; PRIOR APPLICATION NUMBER: DE 10117085.8  
 ; PRIOR FILING DATE: 2001-04-06  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 4  
 ; LENGTH: 3248  
 ; TYPE: DNA  
 ; ORGANISM: Corynebacterium glutamicum  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (802)..(2538)  
 ; OTHER INFORMATION:  
 US-09-965-825-4  
 Alignment Scores:  
 Pred. No.: 3, 92e-272 Length: 3248  
 Score: 2985.00 Matches: 579  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0  
 US-09-965-825-2 (1-579) x US-09-965-825-4 (1-3248)  
 QY 1 MetAlaHISerTYrAlaGluGluLeuIleAspThrLeuGluAlaGluIysValaIysArg 20  
 Db 802 ATGGCACACAGCTACACGACAAACATTAATGACACTTGGAACTCAAGGTGGAAGCGA 861  
 QY 21 IleTYrGIYLeuValaGIYAspSerLeuAnProIleValaAspAlaValaArgGlnSerAsp 40  
 Db 862 ATTTATGCTTTGGTGGGTGATACACCTTAATCCGATGTGATCTGCGCCATATGAT 921  
 QY 41 IleGluTrpValaHISValaArgAsnGluGluAlaAlaAlaPheAlaAlaGluIysSer 60  
 Db 922 ATTGATGGGTGACGTTGGAATGAGAAAGCGCGCGCTTTCACCGGTGGGAATCG 981  
 QY 61 LeuIleThrGIYGIYLeuAlaValaCysAlaAlaSerCysGIYProGIYAsnThrHISLeu 80  
 Db 982 TTGATCACTGGGAGCTGACAGATGTGCTGCTTCTTGAGTCTTGGTGAACACACACCTG 1041  
 QY 81 IleGluGIYLeuTYrAspSerHISArgAsnGluAlaIysValaLeuValaIleAlaSerHIS 100  
 Db 1042 ATTCAGGCTCTTATATATTCGATCGAATAGGCGCAAGGTGTGGCATTCGCTACCAT 1101  
 QY 101 IleProSerAlaGlnIleGIYSerThrPheGlnGluIThrHISProGluIleLeuPhe 120  
 Db 1102 ATTCGAGTGGCCAGATTTGGTTCAGCTTCTTCGGAAGACGATCGGAGATTTGGTTT 1161  
 QY 121 LysGIYCysSerGIYTYrCysGluMetValaAsnGIYGIYGluGluGluIysGluArgIleLeu 140  
 Db 1162 AAGGAATGCTCTGTTACCGCAAGATGTGATGTGTGACACAGGTGAAGCATTTTGG 1221  
 QY 141 HISHISAlaIleGlnSerThrMetAlaGIYIysGIYValaSerValaValaIleProGIY 160  
 Db 1222 CATCAAGCATTCAGTCCACCATGGCGGTTAAAGGTGTGTGGTGGTATGATTCCTGGT 1281  
 QY 161 AspIleAlaIysGluAspAlaGluIysAspGIYThrTYrSerAsnSerThrIleSerSerGIY 180

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Db 1282 GATATCGTAAAGAGACGACGATGACGTTATTCATTCATTCATTCATTCATTCGTCG 1341
Qy 181 ThrProValValPheProAspProThrGluAlaAlaLeuValGluAlaIleAsnAsn 200
Db 1342 ACTCTGTGGTGGTTCCTCGGATCTCTAAGGCTGACGGCTGGTGGAGCGCATTAACAC 1401
Qy 201 AlaYSerValThrLeuPheCysGlyValGlyValIlyAsnAlaArgAlaGlnValLeu 220
Db 1402 GCTAAGTCTGTCATCTTCTTCTCGCGGTGCGGGCGTGAAGATGCTCGCGCGCGAGTGTG 1461
Qy 221 GluLeuAlaGluValIleYSerProIleGlyHisAlaLeuGlyGlyValGlyValIle 240
Db 1462 GAGTGGCGGAGGATTAATCAACCGATCGCGCATGCGCTGGGTGATACAGATCAATC 1521
Qy 241 GlnHisGlnAsnProPheGluValGlyMetSerGlyLeuLeuGlyValGlyValIle 260
Db 1522 CAGCATGGAATCCGTTGAGGTGCGCATGCTGCGCTGCTGCTGCTGCTGCTGCTGCTG 1581
Qy 261 AspAlaSerAsnGluAlaAspLeuLeuIleLeuLeuGlyThrAspPheProTyrSerAsp 280
Db 1582 GATCGCTCCATGAGCGCGATCTGCTGATTCATTCGATTCGATTCGATTCGATTCGAT 1641
Qy 281 PheLeuProIlyAspAsnValAlaGlnValAspIleAsnGlyValHisIleGlyValArg 300
Db 1642 TTCCTTCTTAAGACAAAGCTTGGCCAGGTGATCAACGATGCGCACATTCGTCGAT 1701
Qy 301 ThrThrValIlyThrProValThrGlyAspValAlaAlaThrIleGluAsnIleLeuPro 320
Db 1702 ACCACGGAGGAGTATCCGATCCGATGATGCTGACAACTCGAATAATTTTGGCT 1761
Qy 321 HisValIlyGlyValIlyThrAspArgSerPheLeuAspArgMetLeuValHisIleGlyVal 340
Db 1762 CATGTGAAGGAAAAACAGATCGTCTTCTTCTTGAATCGGATCTCAAGGACACAGAGCT 1821
Qy 341 LysLeuSerSerValValGlyValThrIlyThrHisAsnValGlyValHisValProIleHis 360
Db 1822 AAGTTGAGCTCGGTGATGAGACGATACACATTAACGTCGAGAGCATGCTGATTCAC 1881
Qy 361 ProGluThrValAlaSerIleLeuAsnGluLeuAlaAspIlyAspAlaValPheThrVal 380
Db 1882 CCTGAATCGTTCCTTATTTTGAACGATGCGGTGAAGATGCGGTGTTTACTGTG 1941
Qy 381 AspThrGlyMetCysAsnValThrHisAlaArgTyrIleGluAsnProGluIlyThrArg 400
Db 1942 GATACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2001
Qy 401 AspPheValGlySerPheArgHisGlyIlyThrMetAlaAsnAlaLeuProHisAlaIleGly 420
Db 2002 GACTTGTGGTTCATTCGCGCACGCGCATGCGTATGCGTTCATTCGATTCGATTCG 2061
Qy 421 AlaGlnSerValAspArgAsnArgGlnValIleAlaMetCysGlyAspArgIlyLeuGly 440
Db 2062 GCGCAAGTGTGATCGAAACCGCGCATGATCGGATGATGCGGATGATGCGGTTGGGC 2121
Qy 441 MetLeuLeuGlyValIleLeuThrValIlyLeuHisGlnLeuProLeuValAlaVal 460
Db 2122 ATGCGCTGGGTGATCTGACCGTTAAGCTGACCAACTTCGCTGAAAGCGTGTGTG 2181
Qy 461 PheAsnAsnSerSerIleGlyMetValIlyLeuGlyMetLeuValGlyValIleProGlu 480
Db 2182 TTTTAAACAACATCTTCTTGGCATGCTGAAAGTTCGATGATGCTGCGGAGGACACGCGAA 2241
Qy 481 PheGlyThrAspHisGlyGluValAsnPheAlaGluIleAlaAlaIleGlyIleVal 500
Db 2242 TTTTGTGCTGACATGAGGAAGTGAATTCGACAGATGCGCGCGCTGCTGATCAAA 2301
Qy 501 SerValArgIleThrAspProIlyLeuValArgGluGlnLeuAlaGluAlaLeuAlaVal 520
Db 2302 TCGGATCCCATCCGATCCGAAAGAAAGTTCGCGAGCATGCTGAGGACATTCGCAAT 2361
Qy 521 ProGlyProValIleAspIleValThrAspProAsnAlaLeuSerIleProThr 540

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Db 2362 CCTGACCTGTATCATCATCATATCTGTCACGAGATCTTAATGCGCTGTCATCCACCAAC 2421
Qy 541 IleThrTPGluGlnValIleMetGlyPheSerIlyValAlaThrArgThrValPheGlyVal 560
Db 2422 ATCACTGGGAAACAGGTTCATGGGATTCAGCAAGCGCGCACCCGAAACCGTCTTGGTGA 2481
Qy 561 GlyValGlyAlaMetIleAspLeuAlaArgSerAsnIleArgAsnIleProThrPro 579
Db 2482 GAGATGAGGACGATGATGATCTGCGCGCTTCGAACATTAAGAAATATTCCTAATCCA 2538

RESULT 10
US-09-738-626-1/c
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Alignment Scores:
Pred. No.: 3,966-268 Length: 3309400
Score: 2985.00 Matches: 579
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 9

US-09-965-825-2 (1-579) x US-09-738-626-1 (1-3309400)
Qy 1 MetAlaHisSerTyrAlaGluGlnLeuIleAspThrLeuGluAlaGlnIlyValIlyAsnArg 20
Db 2778504 ATGGCACACACGCTACGCAAGAACATTAATTAATGACCTTGGAAAGCTCAAGGTGAAGGA 2778445
Qy 21 IleTyrGlyLeuValGlyAspSerLeuAsnProIleValAspAlaValArgGlnSerAsp 40
Db 2778444 ATTATGTTGGTGGGTGACAGCCTTAATCCGATCGTGAATGCTGTCGCCCAATTCAGAT 2778385
Qy 41 IleGluThrValHisValArgAsnGluGlnAlaAlaPheAlaAlaGlyValIleGluSer 60
Db 2778384 ATTGAGGGGGTGACGTTCCAAATGAGGAAAGCGGCGGCTTGGCGCGGCGGGAATCG 2778325
Qy 61 LeuIleThrGlyGluLeuAlaValIlyCysAlaAlaSerCysGlyProGlyAsnThrHisLeu 80
Db 2778324 TTGATCACTGGGAGGCTGGCAGATATGCTGCTTCTTGTGTGCTTGAACACACACACTG 2778265
Qy 81 IleGlnIlyLeuTyrAspSerHisArgAsnGlyValIlyValLeuAlaIleAlaSerHis 100
Db 2778264 ATTCAAGGGTCTTATTAATTCGATCGAAATGTCGAAAGGTGTTGGCCATCGCTAAGCAT 2778205

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QY	Db	2777124	TTTAAACAAGCTTCTTGTGGGCAATGGTGAAGTTGAGATGCTCGTGGAGGGACACCGAGAA	2777065
QY	481	PhegiyThraSPH1sglUgluValAspPhe1agluileala1aa1aagly1lelye	500	
Db	2777064	TTTGGTATCTGACNCTANGAGAGTGAATTTCCCAAGAGNTTGGCGCGCTCGCGGATCAA	2777005	
QY	501	SerValArg11eThraSPProLylyValArgglUglu1eual1aglu1aleu1leTy	520	
Db	2777004	TGGTACCCATCACCGATCCAGAAAGATTCCGACAGAGCTAGCTGAGGCTTGGCATAT	2776945	
QY	521	ProgiyProVal1eul1easpl1eVal1ThraSPProem1aleuSer1leProProThr	540	
Db	2776944	CTGGACCTGACTGATGATGATGATGTCACGATCTTAATGGCTGTGATCCACCAAC	2776885	
QY	541	1leThrTPGlu1nVal1eMet1leaspl1eVal1PheSerLy1a1a1aThraThraValPhegi1y	560	
Db	2776884	ATCAGTGGCAACAGGTGATGATGATGATGACAGCAAGCGGCCACCCAGACCGTCTTGGTGA	2776825	
QY	561	GlyValGly1aMet1leaspl1eVal1ArgSeran1leArgan1leProthrPro	579	
Db	2776824	GGAGTAGAGCGATGATGATGATGCGCCGTTCCGAACATAAGAAATATCTACTCCA	2776768	
RESULT 11				
US-10-282-122A-17635				
; Sequence 17635, Application US/10282122A				
; Publication No. US20040029129A1				
; GENERAL INFORMATION:				
; APPLICANT: Wang, Liangsu				
; APPLICANT: Zamudio, Carlos				
; APPLICANT: Malone, Cheryl				
; APPLICANT: Haselbeck, Robert				
; APPLICANT: Ohlsen, Kari				
; APPLICANT: Zyskind, Judith				
; APPLICANT: Wall, Daniel				
; APPLICANT: Trawick, John				
; APPLICANT: Carr, Grant				
; APPLICANT: Yamamoto, Robert				
; APPLICANT: Forsyth, R.				
; APPLICANT: Xu, H.				
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms				
; FILE REFERENCE: EITRA.034A				
; CURRENT APPLICATION NUMBER: US/10/282,122A				
; CURRENT FILING DATE: 2003-02-20				
; PRIOR APPLICATION NUMBER: 60/191,078				
; PRIOR FILING DATE: 2000-03-21				
; PRIOR APPLICATION NUMBER: 60/206,848				
; PRIOR FILING DATE: 2000-05-23				
; PRIOR APPLICATION NUMBER: 60/207,727				
; PRIOR FILING DATE: 2000-05-26				
; PRIOR APPLICATION NUMBER: 60/230,335				
; PRIOR FILING DATE: 2000-09-06				
; PRIOR APPLICATION NUMBER: 60/230,347				
; PRIOR FILING DATE: 2000-09-09				
; PRIOR APPLICATION NUMBER: 60/242,578				
; PRIOR FILING DATE: 2000-10-23				
; PRIOR APPLICATION NUMBER: 60/253,625				
; PRIOR FILING DATE: 2000-11-27				
; PRIOR APPLICATION NUMBER: 60/257,931				
; PRIOR FILING DATE: 2000-12-22				
; PRIOR APPLICATION NUMBER: 60/267,636				
; PRIOR FILING DATE: 2001-02-09				
; PRIOR APPLICATION NUMBER: 60/269,308				
; PRIOR FILING DATE: 2001-02-16				
; Remaining Prior Application data removed - See File Wrapper or PALM.				
; NUMBER OF SEQ ID NOS: 78614				
; SOFTWARE: PatentIn version 3.1				

## Alignment Scores:

Pred. No.: 1.03e-207 Length: 1734  
 Score: 2300.50 Matches: 430  
 Percent Similarity: 86.18% Conservative: 69  
 Best Local Similarity: 74.27% Mismatches: 79  
 Query Match: 77.07% Indels: 1  
 DB: 16 Gaps: 1

US-09-965-825-2 (1-579) x US-10-282-122A-17635 (1-1734)

QY 1 MetLahIasSerYrAlaGluGluLeuIleAphThrLeuGluAlaGlnGlyValIleArg 20  
 Db 1 ATGGCAAAAATTTTGGCGAAACAATCGTAGAACCTTGGAAACCAAGAGTAAAGCGC 60  
 QY 1 ILeThrGlyLeuValAlaGlyAspSerLeuAphProIleValAspAlaValAlaGlnSerAsp 40  
 Db 61 ATCTATGTTGGTGGAGATAGCTCAACCGATCGTAGTCAGTACGCACTCCCAAC 120  
 QY 41 ILeGluTrpValHsValArgAsnGluAlaAlaAphAlaAlaGlyAlaGlnSer 60  
 Db 121 ATCGAATGATCCAGTCGCGCAATGAGAAACAGCAGCTTCGCAAGAGCAAGAAC 180  
 QY 61 LeuIleThrGlyGluLeuValAlaCysAlaAlaSerCysGlyTrpGlyAsnThrHsLeu 80  
 Db 181 CTGCTCAACCGCGCACTGCTGTGTGACGCTCTCCGCGCCCTGGAAATACCACTC 240  
 QY 81 ILeGlnGlyLeuValAspSerHsArgAsnGlyAlaValIleValAlaIleAlaSerHs 100  
 Db 241 GTCCAAAGGACTTTAGACGCAACCAAGCGCGCAAGAGTACCTGCAATGCAAGCAAC 300  
 QY 101 ILeProSerAlaGlnIleGlySerThrPhePheGlnGluThrHsProGluIleLeuPhe 120  
 Db 301 ATTCCCTCAACGCAATCGGCTCATTTCTTCCAGAAACCCCAAGCCCTCTT 360  
 QY 121 LysGluCysSerGlyTrpCysGluMetValAsnGlyGlyGlnGlyGluArgIleLeu 140  
 Db 361 GCTAGTGTCTCGGCTACTGCGAAATGCTTAACCTGCACTCCAGGAGGAGTCACTTGG 420  
 QY 141 HsHsAlaAlaIleGlnSerThrMetAlaGlyValGlyValSerValValIleProGly 160  
 Db 421 CACCAACGCAATCGATCAGCAATGCTGCGCAAGCGCTATCCGCTGCTCTCCACAGC 480  
 QY 161 AspIleAlaValGlyAspAlaGlyAspGlyThrTrpSerAsnSerThrIleSerSerGly 180  
 Db 481 GATGTGACATGCAAGACGTGAGACACACCTTCAACCGGTTCGCGATCTCCACGCA 540  
 QY 181 ThrProValValPheProAspProThrGluAlaAlaAlaLeuValGluAlaIleAsnAsn 200  
 Db 541 CGTCCCATCATGTACCCAGACCCAGCTGAGCGCGCTGACCTTGTCAAGCCATCAACGAG 600  
 QY 201 AlaIleSerValIleThrLeuPheCysGlyAlaGlyValIleValAsnAlaArgAlaGlnValLeu 220  
 Db 601 GCCAAACCGTCACTTGTGTTCGCGTCCGCGCTGCGCTACGCCCGCAAGAGTCTTC 660  
 QY 221 GluLeuAlaGluValIleLeuSerProIleGlyHsAlaLeuGlyGlyValGlyLeuTrpIle 240  
 Db 661 GAATCCGAGAAAGATCAAGCAACCTCCGCAACGCGCTCCGCGGAAATATGATACATC 720  
 QY 241 GlnHsGluAsnProPheGluValAlaGlyMetSerGlyLeuLeuGlyTrpGlyValaCysVal 260  
 Db 721 CAGTAGCAACAACCTTTCGATGAGTGGGCAATGTCGCGCTGCTGCGGTACGAGCCCTGCAC 780  
 QY 261 AspAlaSerAsnGluAlaAspLeuLeuIleLeuLeuGlyTrpAspPheProTrpSerAsp 280  
 Db 781 GACCTTCACAGACGCGACCTGTGTATCTCTCCGCAACGCACTTCCCTTACACAGAC 840  
 QY 281 PheLeuProLysAspAsnValAlaGlnValAlaAspIleAsnGlyAlaHsIleGlyValArg 300  
 Db 841 TTCCTTCCAGCAAGAGCTTTCACATGATCAATCAACGCTCCACATGCGCCGCC 900  
 QY 301 ThrThrValIleTrpProValIleGlyAspValAlaAlaThrIleGluAsnIleLeuPro 320  
 Db 901 ACCGCAATCAACGCAACCTGTGTGTGGCACTTCCGCGCAATTTGAAATCATCTTGGCG 960

QY 321 HsValIleGlyValIleThrAspArgSerPheLeuAspArgMetLeuValHsIleGluArg 340  
 Db 961 CACATCGAGAAAGATCGACCGCTTCTCTCCACCGCAATGCTGAAAGACATCACCGC 1020  
 QY 341 LysLeuSerSerValValGluThrTrpThrHsAsnValGluValHsValProIleHs 360  
 Db 1021 AAGCTTAACGACGTGATCGAGCGCTCAACCTCAGCGGTGAGAAAGCACACCCCTATCCAC 1080  
 QY 361 ProGluTrpValAlaSerIleLeuAsnGluLeuAlaAspLysAspAlaValPheThrVal 380  
 Db 1081 CCAGAAATTTGGCGCAACATTATGACGAAATCCCGCGCAAGATGCCGATTTACCACTC 1140  
 QY 381 AspThrGlyMetCysAsnValTrpHsAlaArgTrpIleGluAsnProGluGlyThrArg 400  
 Db 1141 GATACCGCATGTCCACAGTTGGGGGTCTGCTCAATC---ACCTTAATGGCAAGCT 1197  
 QY 401 AspPheValGlySerPheArgHsGlyThrMetAlaAsnAlaLeuProHsAlaIleGly 420  
 Db 1198 GAATGATCGGCTGCTCCGCAAGCAACATGCGCAATGCGCTGCAAGGCTATCGGC 1257  
 QY 421 AlaGlnSerValAspArgAsnArgGlnValIleAlaMetCysGlyAspGlyGlyLeuGly 440  
 Db 1258 GCATCTGCTGTACCCAGACGTCAGGTTGTCACTTCTGCGCATGTGACCTCGC 1317  
 QY 441 MetLeuLeuGlyGluLeuLeuThrValIleLeuHsIleGlnLeuProLeuValAlaVal 460  
 Db 1318 ATGCTCATGGCGAGCTGCTCACTTTAAGCTGCAACCTTCTTAATTAAGACTGTTCG 1377  
 QY 461 PheAsnAsnSerSerLeuGlyMetValIleLeuGluMetLeuValGluGlyGlnProGlu 480  
 Db 1378 TTTAAACAATCTCTGCTGGGATGTCAGTGAAGTGGTTCAGGGGATCCAGAG 1437  
 QY 481 PheGlyThrAspHsGlyGluValAsnPheAlaGluIleAlaAlaAlaGlyIleLys 500  
 Db 1438 CACGAACTGATCAATGACATGTGACTTGTGATGCCATGCTGTGCAAGGCTATGAG 1497  
 QY 501 SerValArgIleThrAspProLysValArgGluGlnLeuAlaGluAlaLeuAlaTrp 520  
 Db 1498 CACATTAAGATTAAGACCCAGCTTAAGCAAGTCAAGCAAGCTTCAAGCAAGCTTTGATTAT 1557  
 QY 521 ProGlyProValLeuIleAspIleValIleThrAspProAsnAlaLeuSerIleProProThr 540  
 Db 1558 GAGGCTCTGTGCTGATCGATCATCATCATCACTCAACCTTGTGTGATCCACCGAAC 1617  
 QY 541 ILeThrTrpGluGlnValMetGlyPheSerLysAlaAlaThrArgThrValPheGlyGly 560  
 Db 1618 ATCAGATGATGATGATGATGAGGCTTCTCTGTCGACCTACGCGCATGTTTCTGGTGGC 1677  
 QY 561 GlyValGlyAlaMetIleAspLeuAlaArgSerAsnIleArgAsnIleProThrPro 579  
 Db 1678 GCGGTGGCCACATGTAGATATGCGAAGTCAATCTGTACATTCAGAACCA 1734

RESULT 12  
 US-10-156-761-2067  
 Sequence 2067, Application US/10156761  
 Publication No. US20030119018A1  
 GENERAL INFORMATION:  
 APPLICANT: OMDRA, SATOSHI  
 APPLICANT: IKEDA, HARUO  
 APPLICANT: ISHIKAWA, JUN  
 APPLICANT: HORIKAWA, HIROSHI  
 APPLICANT: SHIBA, TADAYOSHI  
 APPLICANT: SAKAKI, YOSHIYUKI  
 APPLICANT: HATTORI, MASAHIRA  
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 FILE REFERENCE: 249-262  
 CURRENT APPLICATION NUMBER: US/10/156,761  
 PRIOR FILING DATE: 2002-05-29  
 PRIOR APPLICATION NUMBER: JP 2001-204089  
 PRIOR FILING DATE: 2001-05-30  
 PRIOR APPLICATION NUMBER: JP 2001-272697  
 PRIOR FILING DATE: 2001-08-02







APPLICANT: SAKAKI, YOSHIYUKI  
 APPLICANT: HATORI, MASAHIRA  
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 FILE REFERENCE: 249-262  
 CURRENT APPLICATION NUMBER: US/10/156,761  
 CURRENT FILING DATE: 2002-05-29  
 PRIOR APPLICATION NUMBER: JP 2001-204089  
 PRIOR FILING DATE: 2001-05-30  
 PRIOR APPLICATION NUMBER: JP 2001-272697  
 PRIOR FILING DATE: 2001-08-02  
 NUMBER OF SEQ ID NOS: 15109  
 SEQ ID NO 1  
 LENGTH: 9025608  
 TYPE: DNA  
 ORGANISM: Streptomyces avermitilis  
 FEATURES:  
 NAME/KEY: misc feature  
 LOCATION: (4187715)  
 OTHER INFORMATION: a, t, c, g, other or unknown  
 US-10-156-761-1

Alignment Scores:  
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 Score: 1746.00 Matches: 338  
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 Best Local Similarity: 58.68% Mismatches: 145  
 Query Match: 58.49% Indels: 4  
 DB: 15 Gaps: 4

US-09-965-825-2 (1-579) x US-10-156-761-1 (1-9025608)

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 Db 2532265 AAGCTCGCGCTGCGCGGCTCTGCGGAGGAACTCCACCTATCAACGAGCTG 2532206  
 QY 85 TyrAspSerHisArgAsnGlyAlaValAlaValIleAlaAlaSerHisIleProSerAla 104  
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 QY 145 GlnSerThrMetAlaGlyValGlyValSerValValIleProGlyAspIleAlaVal 164  
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 QY 185 PheProAspProThrGluAlaAlaAlaLeuValGluAlaIleAsnAlaValSerVal 204  
 Db 2531908 CGGCGCGCGCACACGAGATGACAGAGCTCGTGGGTGATGACGCGGCGGACAGGTC 2531849  
 QY 205 ThrLeuPheCysGlyAlaGlyValAlaValAsnAlaArgAlaGlnValLeuGluLeuAlaGlu 224  
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Db 2531848 ACCCTTCTTCGCGGACGCGGCGGCTGCGACCGCGGAGTCAATGAGTCCCGGAG 2531789  
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 Db 2531788 AAGATCAAGTCCCGGTGCGGACGCGCTGCGGGGAGAGAGTGAATCAATACAGAAC 2531729  
 QY 245 ProPheGluValGlyMetSerGlyLeuLeuGlyTyrGlyAlaCysValAspAlaSerAsn 264  
 Db 2531728 CCGTACGACGTCGCGCATGAGCGGGCTCTCGGTACAGGTGCGGCTACAGAGCCACCAAC 2531669  
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 QY 285 Asp---AsnValAlaGlnValAspIleAsnGlyAlaHisIleGlyValArgTyrThrVal 303  
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 QY 464 SerSerLeuGlyMetValLysValGluMetLeuValGluGlnProGluPheGlyThr 483  
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 QY 544 GluGlnValMetGlyPheSerLysAlaAlaThrArgThrAlaPheGlyGlyValGly 563  
 Db 2530831 GAGATGTGACAGGCTTCCGCTGCTCGCTCAAGATGATCTTCGACGCGGCGGCTGGC 2530772  
 QY 564 AlaMetIleAspLeuAlaArgSerAsnIleArgAsnIleProThrPro 579  
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US-09-965-825-3

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US-09-965-825-2 (1-579) x US-09-965-825-3 (1-875)

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QY      147  ThrMetAlaGIyLYeGIyValSerValValIleProGIyAspIleAlaIyGIuAsp 166
Db      61  ACCATGGCGGGTAAAGGTGTGCTGTGTAGTATTCCTGTGTATTCGCTAAGAGAGAC 120

QY      167  AlaGIyAspGIyThrTySerAsnSerThrIleSerSerGIyThrProValIlePhePro 186
Db      121  GCAGGTGAAGGTACTATTTCATATTCACATTTCTTCTGCACTCTGTGTGTCCG 180

QY      187  AspProThrGIuAlaAlaIleuValGIuAlaIleAsnAsnAlaIySerValThrIleu 206
Db      181  GATCTTACTGAGGTGAGCGCTGTGTGAGCGATTAACAAGCTAAGTGTCTCACTTGG 240

QY      207  PheCyseGIyAlaGIyValIyAsnAlaArgAlaGIuValIleuGIuLeuAlaGIuIySile 226
Db      241  TTCGCGGTGCGGGCGTGAAGATGCTCGCGCGAGTGTGAGTGTGCGGAGAGAGATT 300

QY      227  LysSerProIleGIyHISAlaLeuGIyGIyIySerIleGIyHISGIuAsnProPhe 246
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QY      247  GluValGIyMetSerGIyLeuLeuGIyTyGIyAlaCyValAspAlaSerAsnGIuAla 266
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QY      287  ValAlaGIuValaAspIleAsnGIyAlaHISIleGIyArgArgThrThrValIySleTyPro 306
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QY      327  AsparSerPheLeuAspArgMetLeuIyAlaHISGIuArgIySleuSerSerValIle 346
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QY      347  GluThrTyThrHISAsnValGIuIyHISValProIleHISProGIuTyValAlaSer 366
Db      661  GAGACGTACACACATACGTGAGAGCATGTGCTTATTCACCTGATATACGTGGCTCT 720

QY      367  IleuAsnGIuLeuAlaAspIyAspAlaValPheThrValAspThrGIyMetCyAsn 386
Db      721  ATTTTGAACGAGCTGGCGGATTAAGATGCGGTGTTTACTGTGATACCGGCATGTGCAT 780

QY      387  ValTrpHISAlaArgTyIleGIuAsnProGIuGIyThrArgAspPheValGIySerPhe 406
Db      781  GTGTGGCATGAGGATCATCGAAGATCCGAGAGGGAACGCGCACTTGTGGTTCAATTC 840

QY      407  ArgHISGIyThrMetAlaAsnAlaLeuProHIS 417
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 Job time : 12210 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: January 15, 2005, 08:14:27 ; Search time 1662.44 Seconds  
(without alignments)  
11226.071 Million cell updates/sec

Title: US-09-965-825-4

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Scoring table: IDENTITY\_NNC  
Gapop 10.0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%

Listing first 45 summaries

## Database:

Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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3	2160	66.5	2160	9	US-09-965-825-1
4	2160	66.5	2160	15	US-10-143-856-3
5	2160	66.5	2160	15	US-10-078-167-4
6	2160	66.5	2160	15	US-10-336-049-4
7	2160	66.5	2160	15	US-10-091-342-4
8	2160	66.5	2160	16	US-10-686-736-4
9	1860	57.3	1860	17	US-10-781-014-85
10	1737	53.5	1737	9	US-09-738-626-2873
11	944	29.1	944	17	US-10-781-014-89
12	875	26.9	875	9	US-09-965-825-3

13	875	26.9	875	15	US-10-143-856-5	Sequence 5, Appl1
14	875	26.9	875	15	US-10-078-167-6	Sequence 6, Appl1
15	875	26.9	875	15	US-10-336-049-6	Sequence 6, Appl1
16	875	26.9	875	15	US-10-091-342-6	Sequence 6, Appl1
17	875	26.9	875	15	US-10-686-736-6	Sequence 6, Appl1
18	822	25.3	1140	9	US-09-738-626-2872	Sequence 2872, Ap
19	813.8	25.1	1734	16	US-10-282-122A-17635	Sequence 17635, A
20	721.4	22.2	1422	9	US-09-965-825-12	Sequence 12, Appl
21	613	18.9	613	9	US-09-965-825-7	Sequence 7, Appl1
22	551	17.0	552	17	US-10-781-014-87	Sequence 87, Appl
23	523	16.1	9025608	15	US-10-156-761-1	Sequence 1, Appl1
24	522.6	16.1	1740	15	US-10-156-761-2067	Sequence 2067, Ap
25	475	14.6	475	9	US-09-965-825-6	Sequence 6, Appl1
26	397.6	12.2	1710	15	US-10-369-493-3295	Sequence 3295, A
27	397.6	12.2	1710	15	US-10-369-493-33670	Sequence 33670, A
28	397.6	12.2	1710	15	US-10-369-493-40028	Sequence 40028, A
29	381	11.7	1737	16	US-10-282-122A-12285	Sequence 12285, A
30	380.4	11.7	1737	16	US-10-282-122A-33768	Sequence 33768, A
31	369.4	11.4	1722	16	US-10-282-122A-32583	Sequence 32583, A
32	365.4	11.2	1767	16	US-10-282-122A-11945	Sequence 11945, A
33	363.2	11.2	1728	16	US-10-282-122A-14452	Sequence 14452, A
34	361.2	11.1	1716	16	US-10-282-122A-23384	Sequence 23384, A
35	352.4	10.8	1722	16	US-10-282-122A-41795	Sequence 41795, A
36	350.4	10.8	1706	16	US-10-282-122A-19600	Sequence 19600, A
37	345.2	10.6	1806	16	US-10-282-122A-13519	Sequence 13519, A
38	344.8	10.6	1719	9	US-09-815-242-9838	Sequence 9838, Ap
39	344.8	10.6	1719	16	US-10-282-122A-23976	Sequence 23976, A
40	341	10.5	1482	9	US-09-738-626-2874	Sequence 2874, Ap
41	305.2	9.4	1719	9	US-09-815-242-6012	Sequence 6012, Ap
42	305.2	9.4	1719	13	US-10-096-571-1	Sequence 1, Appl1
43	305.2	9.4	1719	14	US-10-076-416-1	Sequence 1, Appl1
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## ALIGNMENTS

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US-09-965-825-4  
Sequence 4, Application US/09965825  
Patent No. US2002015099A1  
GENERAL INFORMATION:  
APPLICANT: DUSCH, Nicole  
APPLICANT: THIERBACH, Georg  
TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENIC ACID US  
FILE REFERENCE: 21354USOX  
CURRENT FILING DATE: 2001-10-01  
CURRENT FILING DATE: 2001-09-01  
PRIOR APPLICATION NUMBER: DE 10048604.5  
PRIOR FILING DATE: 2000-09-30  
PRIOR APPLICATION NUMBER: DE 10117085.8  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patent version 3.1  
SEQ ID NO 4  
LENGTH: 3248  
TYPE: DNA  
ORGANISM: Corynebacterium glutamicum  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (802)..(2538)  
OTHER INFORMATION:  
US-09-965-825-4

Query Match 100.0%; Score 3248; DB 9; Length 3248;  
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Matches 3248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1501 CTGGGTGTGAAGCAATCAACGATGAAGATCCGTTGAGGTGGGCAATGTTGGCTG 1560  
Qy 1561 CTGGGTGAAGCGGCTCTGGTGAATGGTCAATGAGCGGATCTGTTATTTGGGT 1620  
Db 1561 CTGGGTGAAGCGGCTCTGGTGAATGGTCAATGAGCGGATCTGTTATTTGGGT 1620  
Qy 1621 ACGGATTTCCCTTATCTGATTTCTCTTAAGAACAAGTTGCCAGGTGAATCAAC 1680  
Db 1621 ACGGATTTCCCTTATCTGATTTCTCTTAAGAACAAGTTGCCAGGTGAATCAAC 1680  
Qy 1681 GGTGCGCAATTTGTGACGTAACAAGGTGAAGTCCCGTGAACGCGTGAATTTGCGA 1740  
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Db 1741 ACAATCGAAATATTTTGGCTCATGTGAAGAAACAGATCTCTTCTTGAATCG 1800  
Qy 1801 ATGCTCAAGGCAACAGAGCGTAAGTTGAGCTGGGTGAAGACGTAACAATACGTC 1860  
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Qy 1861 GAAAGCATGTGCTTATTCACCTGATTAAGTTGCTTATTTGAACGAGCTGGCGAT 1920  
Db 1861 GAAAGCATGTGCTTATTCACCTGATTAAGTTGCTTATTTGAACGAGCTGGCGAT 1920  
Qy 1921 AAGATGCGGTGTTTATCTGTGATACCGGCAATGTCATGTCGATGCGAGTATC 1980  
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Db 1981 GAGATTCGAGAGGAACGCGCACTTTGTGGGTGATTCGCGCAACGCAAGTGGTAT 2040  
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Db 2041 GCGTTGCTCATGCAATTTGTGCAAAAGTGTGATCAACCGGCAAGTGAATCGCATG 2100  
Qy 2101 TGTGCGATGTGTTTGGGCAATGCTGTGGGTGAGCTTGAACGTTAAGCTGACCA 2160  
Db 2101 TGTGCGATGTGTTTGGGCAATGCTGTGGGTGAGCTTGAACGTTAAGCTGACCA 2160  
Qy 2161 CTTTGGCTGAAGCGTGTGTGTTTAAACAAGTTCTTTGGGCGATGTGAAGTGAAGT 2220  
Db 2161 CTTTGGCTGAAGCGTGTGTGTTTAAACAAGTTCTTTGGGCGATGTGAAGTGAAGT 2220

QY	2221	CTCGGAGAGGGA	CAGACCAGAA	TTTGGATCTCA	CCATGAGAA	GGAAATTTGGCAGAGATT	2280
Db	2221	CTCGGAGAGGGA	CAGACCAGAA	TTTGGATCTCA	CCATGAGAA	GGAAATTTGGCAGAGATT	2280
QY	2281	GCGGCGGCTGCGGGATCA	MAATCGGTACG	ATCA	CCGATCCGAA	GGAAAGTTGCGGACGAG	2340
Db	2281	GCGGCGGCTGCGGGATCA	MAATCGGTACG	ATCA	CCGATCCGAA	GGAAAGTTGCGGACGAG	2340
QY	2341	CTAGGTGAGGCA	TTGAGCATTC	CTGGAAC	CTGTATCTGATAT	TCGTACAGGATCTTAAT	2400
Db	2341	CTAGGTGAGGCA	TTGAGCATTC	CTGGAAC	CTGTATCTGATAT	TCGTACAGGATCTTAAT	2400
QY	2401	GCGGCTGATCCCA	CCAAACATCA	CGTGGAA	CAGGTCATGGGATTCAG	GAAGGCGGCGC	2460
Db	2401	GCGGCTGATCCCA	CCAAACATCA	CGTGGAA	CAGGTCATGGGATTCAG	GAAGGCGGCGC	2460
QY	2461	ACCGGAACCGCTCTT	GTGTGAGAGAGTA	GAGAGCATGATCGATCTGG	CCCGTTCCGA	CATA	2520
Db	2461	ACCGGAACCGCTCTT	GTGTGAGAGAGTA	GAGAGCATGATCGATCTGG	CCCGTTCCGA	CATA	2520
QY	2521	AGGAATATTCCTA	CTCCATGATGATTA	CA	CCTGCTGTTCTCAT	TTGACCGGACGCGT	2580
Db	2521	AGGAATATTCCTA	CTCCATGATGATTA	CA	CCTGCTGTTCTCAT	TTGACCGGACGCGT	2580
QY	2581	TAACTGCCAACAT	TTTCCAGATGGGAGCTCA	CGCCGGTGGCCCAT	GTAGATTTGCCCTGCGTC		2640
Db	2581	TAACTGCCAACAT	TTTCCAGATGGGAGCTCA	CGCCGGTGGCCCAT	GTAGATTTGCCCTGCGTC		2640
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QY	2821	TCCCGGAGAA	ATTTCCATTTGCGCGATTC	CGGTAGAGATG	GCACAGGCGAC	CGGCGGTT	2880
Db	2821	TCCCGGAGAA	ATTTCCATTTGCGCGATTC	CGGTAGAGATG	GCACAGGCGAC	CGGCGGTT	2880
QY	2881	TGCGGGAAGATAT	CAAGGCTCTGATTTGA	ATGATTCGGGACAT	CGTGAAGTGA	GTCA	2940
Db	2881	TGCGGGAAGATAT	CAAGGCTCTGATTTGA	ATGATTCGGGACAT	CGTGAAGTGA	GTCA	2940
QY	2941	CGGCGACTGCTT	CAGAAATTTGAGTCA	GCATCCGCGAGG	CCCTGGGACAG	CAGGTATCAGGAG	3000
Db	2941	CGGCGACTGCTT	CAGAAATTTGAGTCA	GCATCCGCGAGG	CCCTGGGACAG	CAGGTATCAGGAG	3000
QY	3001	TGTTTACTTTT	CTCGGGGATTTCTTA	TGGCCCGGGA	ATGGTGACAGG	CACACACTGATG	3060
Db	3001	TGTTTACTTTT	CTCGGGGATTTCTTA	TGGCCCGGGA	ATGGTGACAGG	CACACACTGATG	3060
QY	3061	AGCTTCAAGGCT	CTTAAACAACAGCGT	CCAGCACTTGGCGG	CGCTGA	CTTCTGGCGGTT	3120
Db	3061	AGCTTCAAGGCT	CTTAAACAACAGCGT	CCAGCACTTGGCGG	CGCTGA	CTTCTGGCGGTT	3120
QY	3121	CCTCGCGCTG	CGCAGATTTA	CAGA	CGCAATCGATGAGATCG	CAGCGCGTGTATGTT	3180
Db	3121	CCTCGCGCTG	CGCAGATTTA	CAGA	CGCAATCGATGAGATCG	CAGCGCGTGTATGTT	3180
QY	3181	TTTAACGAT	TCCAGCAGATCA	CTCGGAGCAT	GTGCTGAGAA	AGCAGGTGGCAATGACG	3240
Db	3181	TTTAACGAT	TCCAGCAGATCA	CTCGGAGCAT	GTGCTGAGAA	AGCAGGTGGCAATGACG	3240
QY	3241	TGCTGTCT	3248				
Db	3241	TGCTGTCT	3248				

[illegible]



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Db 2778705 TTGCAAGCGGCTGAAACCAACCAAGCTGCCCAGACAGACGGAATCCCAAAAGTGGCA 2778646  
QY 661 TCCCTGTTGGTACCGAGTACCCACCGGGCTGAACTCCCTGGCAGGCGGAGCG 720  
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QY 1561 CTGTGTTAAGCGAGCTGCGGTGATGCGTCAATGAGCGGATGCTGATTTATTTGGGT 1620  
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QY 1681 GTTGCCGACATTTGTTGAGAGTACACAGGTGAAGATATCCGGTGAAGTGTGCTGCA 1740  
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Db 2777505 ATGCTAAGGACACAGAGCGTAAGTTGAGCTCGGTGTGAAGACGTACACATTAAGTTC 2777446  
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QY 2161 CTTCGCTGAAGGCTGTGTGTTTAAACAAGTCTTTGGGCAATGTTGAAGTGAAGATG 2220  
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QY 2521 AAGAAATATTCCTACTCATGATGATTAACCTGTGTCTCATTTGACGCGAGCGGT 2580  
Db 2776785 AAGAAATATTCCTACTCATGATGATTAACCTGTGTCTCATTTGACGCGAGCGGT 2776726  
QY 2581 TTAATGCGCAAACTTTCAGAGATGAGCTACAGCGCGGTGCCATGAGATGCTGCGCTC 2640  
Db 2776725 TTAATGCGCAAACTTTCAGAGATGAGCTACAGCGCGGTGCCATGAGATGCTGCGCTC 2776666  
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## RESULT 3

US-09-965-825-1  
 ; Sequence 1, Application US/09965825  
 ; Patent No. US2002015099A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DUSCH, Nicole  
 ; APPLICANT: THOMAS, Hermann  
 ; APPLICANT: THIERSCH, Georg  
 ; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENIC ACID U  
 ; FILE REFERENCE: 21354US0X  
 ; CURRENT APPLICATION NUMBER: US/09/965,825  
 ; PRIOR APPLICATION NUMBER: DE 10048604.5  
 ; PRIOR FILING DATE: 2000-09-30  
 ; PRIOR APPLICATION NUMBER: DE 10117085.8  
 ; PRIOR FILING DATE: 2001-04-06  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 2160  
 ; TYPE: DNA  
 ; ORGANISM: Corynebacterium glutamicum  
 ; FEATURES:  
 ; NAME/KEY: CDS  
 ; LOCATION: (327)..(2063)  
 ; OTHER INFORMATION:  
 ; NAME/KEY: -35\_signal  
 ; LOCATION: (1227)..(1232)  
 ; OTHER INFORMATION:  
 ; NAME/KEY: -10\_signal  
 ; LOCATION: (256)..(261)  
 ; OTHER INFORMATION:  
 ; US-09-965-825-1

Query Match 66.5%; Score 2160; DB 9; Length 2160;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 2336 AGCAGTACGCTGAGGATTTGAGATTTCTGAGATGAGATGAGATGAGATGAGATGAGT 2395  
 Db 1861 AGCAGTACGCTGAGGATTTGAGATTTCTGAGATGAGATGAGATGAGATGAGATGAGT 1920  
 QY 2396 CTAAATGCTGCTGAGATTTGAGATTTCTGAGATGAGATGAGATGAGATGAGATGAGT 2455  
 Db 1921 CTAAATGCTGCTGAGATTTGAGATTTCTGAGATGAGATGAGATGAGATGAGATGAGT 1980  
 QY 2456 CGCGCAACCGGATTTGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGT 2515  
 Db 1981 CGCGCAACCGGATTTGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGT 2040  
 QY 2516 ACATAAGATATTTCTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGT 2575  
 Db 2041 ACATAAGATATTTCTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGT 2100  
 QY 2576 GCGCTTAATGCGCAATTTTCAAGATGAGATGAGATGAGATGAGATGAGATGAGT 2635

Db 2101 GCGCTTAATGCGCAATTTTCAAGATGAGATGAGATGAGATGAGATGAGATGAGT 2160  
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 US-10-143-856-3  
 ; Sequence 3, Application US/10143856  
 ; Publication No. US20030109014A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BURKE, KEVIN  
 ; APPLICANT: DUNICAN, L.K.  
 ; APPLICANT: MCCORMACK, ASHLING  
 ; APPLICANT: MCCORMACK, CLIONA  
 ; APPLICANT: MOCKEL, BETTINA  
 ; APPLICANT: THIERBACH, GEORG  
 ; TITLE OF INVENTION: Process for the fermentative preparation of  
 ; TITLE OF INVENTION: with amplification of the tkt gene  
 ; FILE REFERENCE: MAS/021123/282432  
 ; CURRENT APPLICATION NUMBER: US/10/143,856  
 ; CURRENT FILING DATE: 2002-05-14  
 ; PRIOR APPLICATION NUMBER: 09/986,649  
 ; PRIOR FILING DATE: 17-03-2000  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 2160  
 ; TYPE: DNA  
 ; ORGANISM: Corynebacterium glutamicum  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (327)..(2063)  
 ; OTHER INFORMATION: poxb  
 US-10-143-856-3  
 Query Match 66.5%; Score 2160; DB 15; Length 2160;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 476 TTAGAGGCAATTCGAGAGTCACTTTTGTGGGGTGGGGGTCTAAATTTGGCAGATTT 535  
 Db 1 TTAGAGGCAATTCGAGAGTCACTTTTGTGGGGTGGGGGTCTAAATTTGGCAGATTT 60  
 QY 536 CGAGGGACAGACAGAGCGTGCACAGATTTTAAATAGCGATCGTGGGATCTGTGT 595  
 Db 61 CGAGGGACAGACAGAGCGTGCACAGATTTTAAATAGCGATCGTGGGATCTGTGT 120  
 QY 596 TTGTTTCAAGGGGTGAAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 655  
 Db 121 TTGTTTCAAGGGGTGAAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 180  
 QY 656 GGGCATCCCTGTTGGTACCGAGTACCCACCGGGGCTGAAACTCCCTGGCAGGGGGCG 715  
 Db 181 GGGCATCCCTGTTGGTACCGAGTACCCACCGGGGCTGAAACTCCCTGGCAGGGGGCG 240  
 QY 716 AAGCGTGGCAACACTGGAATTTAAGAGCAATTTAAGATGCGACCAAGTTAGGCAAC 775  
 Db 241 AAGCGTGGCAACACTGGAATTTAAGAGCAATTTAAGATGCGACCAAGTTAGGCAAC 300  
 QY 776 AATAAGCATTAAGTGAAGAGTTCAAGTGGCAACAGCTACGCAACCAATTAATTGACA 835  
 Db 301 AATAAGCATTAAGTGAAGAGTTCAAGTGGCAACAGCTACGCAACCAATTAATTGACA 360  
 QY 836 CTTTGAAGCTCAAGGTGGAAGCAATTTAAGTGTGGGTTGACAGCCTTAATTCGA 895  
 Db 361 CTTTGAAGCTCAAGGTGGAAGCAATTTAAGTGTGGGTTGACAGCCTTAATTCGA 420  
 QY 896 TCGTGAATGCTGTCGCAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 955  
 Db 421 TCGTGAATGCTGTCGCAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 480  
 QY 956 CCGGCTTTGACGCGGTGCGGATGTTGATGATCACTGGGAGTGGCAGTATGCTGCTT 1015  
 Db 481 CCGGCTTTGACGCGGTGCGGATGTTGATGATCACTGGGAGTGGCAGTATGCTGCTT 540



Db 61 CGAGGACCAAGGAGGTCGCCAAGATGTTAAATAGCGATCGGTGGCATCTGTGT 120  
Qy 596 TTGGTTTGAACGGGCTGAAACCAACGACATGCGCCAGCAACGAGAAATCCCAAGT 655  
Db 121 TTGGTTTGAACGGGCTGAAACCAACGACATGCGCCAGCAACGAGAAATCCCAAGT 180  
Qy 656 GGGGATCTCTGTTTGTACCGAGTACCAACCGGGCTGAAACTCCCTGGCAGCGGGCG 715  
Db 181 GGGGATCTCTGTTTGTACCGAGTACCAACCGGGCTGAAACTCCCTGGCAGCGGGCG 240  
Qy 716 AAGGTGGCAACATCTGAATTTAAGACCAATTTGAAGTGGCAACCAAGTTAAGCAAC 775  
Db 241 AAGGTGGCAACATCTGAATTTAAGACCAATTTGAAGTGGCAACCAAGTTAAGCAAC 300  
Qy 776 AATAGCATTAAGTTGAGAGTTGAGAGTGGCAACAGCTACGCGAACAATTAATGACA 835  
Db 301 AATAGCATTAAGTTGAGAGTTGAGAGTGGCAACAGCTACGCGAACAATTAATGACA 360  
Qy 836 CTTTGAAAGCTCAAGGTGTGAAGCAATTAATGTTTGTGTGTGACAGCCTTAATCGA 895  
Db 361 CTTTGAAAGCTCAAGGTGTGAAGCAATTAATGTTTGTGTGTGACAGCCTTAATCGA 420  
Qy 896 TCGTGATGCTGTCCGCAATCAAGATTTGAGTGGGTGCAAGTTGCAAAATGAGAGCGG 955  
Db 421 TCGTGATGCTGTCCGCAATCAAGATTTGAGTGGGTGCAAGTTGCAAAATGAGAGCGG 480  
Qy 956 CGGCGTTTGAAGCGGCTGCGGAATCTGTGATCACTGGGAGCTGGCAGTATGTCCTT 1015  
Db 481 CGGCGTTTGAAGCGGCTGCGGAATCTGTGATCACTGGGAGCTGGCAGTATGTCCTT 540  
Qy 1016 CTGTGTGCTGTGAACAACAACCTGTGATCAAGGTCTTTATGATTCGATCGAAATGAG 1075  
Db 541 CTGTGTGCTGTGAACAACAACCTGTGATCAAGGTCTTTATGATTCGATCGAAATGAG 600  
Qy 1076 CGAAGGTGTGGCCATGCTAGCAATTCGAGTGGCCAGATTTGTTGCACTTCTTCC 1135  
Db 601 CGAAGGTGTGGCCATGCTAGCAATTCGAGTGGCCAGATTTGTTGCACTTCTTCC 660  
Qy 1136 AGGAAACGATCCGAGATTTGTTTAAAGAAATGCTCTGTGTTACTGGAGATGAGTATG 1195  
Db 661 AGGAAACGATCCGAGATTTGTTTAAAGAAATGCTCTGTGTTACTGGAGATGAGTATG 720  
Qy 1196 GTGTGTGAGAGGTGAACGATTTTGCATCAAGCTGATTCAGTCCACCATGGCGGTAAAG 1255  
Db 721 GTGTGTGAGAGGTGAACGATTTTGCATCAAGCTGATTCAGTCCACCATGGCGGTAAAG 780  
Qy 1256 GTGTGTGAGAGGTGAACGATTTTGCATCAAGCTGATTCAGTCCACCATGGCGGTAAAG 1315  
Db 781 GTGTGTGAGAGGTGAACGATTTTGCATCAAGCTGATTCAGTCCACCATGGCGGTAAAG 840  
Qy 1316 AATTCATTTCCATATTTCTTTCGCACTCTGTGTGTTCGCGATCTTACTGAGGCTG 1375  
Db 841 AATTCATTTCCATATTTCTTTCGCACTCTGTGTGTTCGCGATCTTACTGAGGCTG 900  
Qy 1376 CAGCGCTGTGAGAGGTGAACGATTTAAGCTGCTGCTGTTGTTCTGCGGTGCGGCG 1435  
Db 901 CAGCGCTGTGAGAGGTGAACGATTTAAGCTGCTGCTGTTGTTCTGCGGTGCGGCG 960  
Qy 1436 TGAAGAATGCTCCGCGCAGGTGTGAGATTTGGCGGAGAAATTAATCAACGATGGGCG 1495  
Db 961 TGAAGAATGCTCCGCGCAGGTGTGAGATTTGGCGGAGAAATTAATCAACGATGGGCG 1020  
Qy 1496 ATGCGCTGTGAGAGGTGAACGATTTAAGCTGCTGCTGTTGAGGTGCGGATGCTG 1555  
Db 1021 ATGCGCTGTGAGAGGTGAACGATTTAAGCTGCTGCTGTTGAGGTGCGGATGCTG 1080  
Qy 1556 GCGTGTGTTGTTACGCGCTGTGCTGATGCTGCTCAATGAGCGGATCTGCTGATTTAT 1615  
Db 1081 GCGTGTGTTGTTACGCGCTGTGCTGATGCTGCTCAATGAGCGGATCTGCTGATTTAT 1140  
Qy 1616 TGGGTACGATTTCCCTTATTTCTGATTTCTTCTTAAAGCAAGTTGCCAGGTGATTA 1675

Db 1141 TGGGTACGATTTCCCTTATTTCTGATTTCTTCTTAAAGCAAGCTTGCCAGGTGATTA 1200  
Qy 1676 TCAACGGTGGCAGATTTGCTGACGTACCAAGGTGAAGTATCCGGTGAATGTTG 1735  
Db 1201 TCAACGGTGGCAGATTTGCTGACGTACCAAGGTGAAGTATCCGGTGAATGTTG 1260  
Qy 1736 CTGCAACATCGAAATATTTTGTCTCATGTGAGGAAAAAAGATGCTTCTTCTTG 1795  
Db 1261 CTGCAACATCGAAATATTTTGTCTCATGTGAGGAAAAAAGATGCTTCTTCTTG 1320  
Qy 1796 ATGGAATGCTCAAGGACCAAGAGCTTAAGTGAAGTGGTGGTGAAGATGACATTA 1855  
Db 1321 ATGGAATGCTCAAGGACCAAGAGCTTAAGTGAAGTGGTGGTGAAGATGACATTA 1380  
Qy 1856 ACCTGCAAGAGCATGTCCTTATTCCTGAAATACCTTCTTATTTTGAACGAGCTG 1915  
Db 1381 ACCTGCAAGAGCATGTCCTTATTCCTGAAATACCTTCTTATTTTGAACGAGCTG 1440  
Qy 1916 CGGATTAAGATGCGGTGTTTACTGTGATTAACCGCATGTGCAATGTGTGCAATGCGAGGT 1975  
Db 1441 CGGATTAAGATGCGGTGTTTACTGTGATTAACCGCATGTGCAATGTGTGCAATGCGAGGT 1500  
Qy 1976 ACATCGAATTCGGAGGGAACGCGGACTTTGTGGGTTCATTTCCGCCACGCGACATG 2035  
Db 1501 ACATCGAATTCGGAGGGAACGCGGACTTTGTGGGTTCATTTCCGCCACGCGACATG 1560  
Qy 2036 CTAAATCGTTGCTCATGCGAATTTGTCGCAAAAGTTGATCGAAACCCGACAGTATG 2095  
Db 1561 CTAAATCGTTGCTCATGCGAATTTGTCGCAAAAGTTGATCGAAACCCGACAGTATG 1620  
Qy 2096 CGATGTGTGCGATGAGTGTGTTGGGATCTGTGCGGTGAGCTTGAACGTTAGCTGC 2155  
Db 1621 CGATGTGTGCGATGAGTGTGTTGGGATCTGTGCGGTGAGCTTGAACGTTAGCTGC 1680  
Qy 2156 ACCAATCTTCGCTGAAGGCTGTGTGTTTAAACAAGTCTTTGGGCAAGTGAAGTGG 2215  
Db 1681 ACCAATCTTCGCTGAAGGCTGTGTGTTTAAACAAGTCTTTGGGCAAGTGAAGTGG 1740  
Qy 2216 AGATGCTGTGAGGGAACGCAAGTTTGTACTGACCATGAGGAAGTAATTTGCGAG 2275  
Db 1741 AGATGCTGTGAGGGAACGCAAGTTTGTACTGACCATGAGGAAGTAATTTGCGAG 1800  
Qy 2276 AGATGCTGTGAGGGAATGAAATCGGTACGATCCGATCCGAAAGAAATTTGCGG 2335  
Db 1801 AGATGCTGTGAGGGAATGAAATCGGTACGATCCGATCCGAAAGAAATTTGCGG 1860  
Qy 2336 AGAGCTACTGAGGATTTGGAATCTGTGACCTGTACTGATTCATATCTGACAGGATC 2395  
Db 1861 AGAGCTACTGAGGATTTGGAATCTGTGACCTGTACTGATTCATATCTGACAGGATC 1920  
Qy 2396 CTAAATGCTGTGATCCCAACCATCAAGTGGGAACAGGTCAATGGATTCAGCAAG 2455  
Db 1921 CTAAATGCTGTGATCCCAACCATCAAGTGGGAACAGGTCAATGGATTCAGCAAG 1980  
Qy 2456 CGGCGCAACCGCTTGTGTGAGAGTGAAGAGCATGATGATGATGATGATGATGATG 2515  
Db 1981 CGGCGCAACCGCTTGTGTGAGAGTGAAGAGCATGATGATGATGATGATGATGATG 2040  
Qy 2516 ACATTAAGAAATATTTCTTCAATCATATGATTAATCACTGCTGTTCATTAAGACGGA 2575  
Db 2041 ACATTAAGAAATATTTCTTCAATCATATGATTAATCACTGCTGTTCATTAAGACGGA 2100  
Qy 2576 GCGCTTAATGCGCAATTTCAAGATGGCACTGACGCGGTGGCCATGAGATTTGCCCT 2635  
Db 2101 GCGCTTAATGCGCAATTTCAAGATGGCACTGACGCGGTGGCCATGAGATTTGCCCT 2160

RESULT 6  
US-10-336-049-4  
; Sequence 4, Application US/10336049  
; Publication No. US20030175911A1  
; GENERAL INFORMATION:  
; APPLICANT: Hans, Stephan

/ APPLICANT: Bathe, Brigitte  
 / APPLICANT: Reith, Alexander  
 / APPLICANT: Thierbach, Georg  
 / APPLICANT: Kreutzer, Caroline  
 / APPLICANT: Mockel, Bettina  
 / TITLE OF INVENTION: Process for the Preparation of L-Amino Acids with Amplification c  
 / TITLE OF INVENTION: the zwf Gene  
 / FILE REFERENCE: 7601/80158  
 / CURRENT APPLICATION NUMBER: US/10/336, 049  
 / CURRENT FILING DATE: 2003-01-30  
 / NUMBER OF SEQ ID NOS: 37  
 / SOFTWARE: PatentIn version 3.1  
 / SEQ ID NO 4  
 / LENGTH: 2160  
 / TYPE: DNA  
 / ORGANISM: Corynebacterium glutamicum  
 / FEATURE:  
 / NAME/KEY: CDS  
 / LOCATION: (327)..(2063)  
 / OTHER INFORMATION: poxb  
 / US-10-336-049-4

Query Match 66.5%; Score 2160; DB 15; Length 2160;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 476 TTAGAGGCGATTCTGTGAGGTCACTTTTGTGGGGTCCGAGGCTTAATTTGGCGAGTTT 535  
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 QY 536 CGAGGCGACAGACAGGCGTCCACGATGTTTAAATAGCGATCGGTGGCATCTGTGT 595  
 DB 61 CGAGGCGACAGACAGGCGTCCACGATGTTTAAATAGCGATCGGTGGCATCTGTGT 120  
 QY 596 TTGGTTTCAGCGGCTGAACCAACCAAGCTCCGACGACGAGGAAATCCCAAAAGT 655  
 DB 121 TTGGTTTCAGCGGCTGAACCAACCAAGCTCCGACGACGAGGAAATCCCAAAAGT 180  
 QY 656 GGGGATCCCTGTTTGTATCGAGTACCAACCCGGGCTGAACCTCCGAGGAGGGGGG 715  
 DB 181 GGGGATCCCTGTTTGTATCGAGTACCAACCCGGGCTGAACCTCCGAGGAGGGGGG 240  
 QY 716 AAGCGTGGCAACAACGATTTTAAAGACAATTTGAAGTCGACCAAGTTAGGCAAC 775  
 DB 241 AAGCGTGGCAACAACGATTTTAAAGACAATTTGAAGTCGACCAAGTTAGGCAAC 300  
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 DB 481 CGGCGTTTGAAGCGCGGTGCGGAATCGTTGATCACTGGGAGCTGGCAGTATGCTCTT 540  
 QY 1016 CTTTGTGCTCTGAAACACACACTGATTCAGGGTCTTTATGATTCGATCGAAATGATG 1075  
 DB 541 CTTTGTGCTCTGAAACACACACTGATTCAGGGTCTTTATGATTCGATCGAAATGATG 600  
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 DB 601 CGAAGGTGGCGATCGCTAGCATATTCGAGTGGCGAGTGGTTGCGAGTTCTTCC 660  
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QY 1196 GTGTGAGCAGGAGTGAACGATTTTGCATCAACGATTCAGTCCACCATGCGGGTAAAG 1255  
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 DB 1081 GCTGTGTTGTTACGCGCGCTGCGTGGATCGTCAATGAGGCGGATCTGCTATCTAT 1140  
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 DB 1321 ATCGATGCTCAAGGCAACAGAGCGTAAAGTGAAGTGGTGTGAGACGTAACACATA 1380  
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 DB 1381 ACGTCAAGAACATGTGCTTATTCACCTGAATACGTTGCTTATTTTGAACGAGCTCG 1440  
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 DB 1441 CGGATTAAGATGGGCTGTATCTGTGATACCGGCAATGTGCAATGTGCGATGCGAGGT 1500  
 QY 1976 ACATCGAATATCCGAGGAGAACGCGCACTTTGTGGGTTCAATCCGCAAGGACGATG 2035  
 DB 1501 ACATCGAATATCCGAGGAGAACGCGCACTTTGTGGGTTCAATCCGCAAGGACGATG 1560  
 QY 2036 CTAATGCTTGCCTCATGCGATTTGTGCGCAAAAGTGTGATCGAAACCGCGAAGTATG 2095  
 DB 1561 CTAATGCTTGCCTCATGCGATTTGTGCGCAAAAGTGTGATCGAAACCGCGAAGTATG 1620  
 QY 2096 CGATGTGTGCGAATGTGTGTTTGGGCACTGTGCTGGGTGAGCTTGTGACCGTTTAACTG 2155  
 DB 1621 CGATGTGTGCGAATGTGTGTTTGGGCACTGTGCTGGGTGAGCTTGTGACCGTTTAACTG 1680  
 QY 2156 ACCAATTCGCGTGAAGGCTGTGTGTTTAAACAACAGTTCTTTGGGCAATGTTGAATTTG 2215  
 DB 1681 ACCAATTCGCGTGAAGGCTGTGTGTTTAAACAACAGTTCTTTGGGCAATGTTGAATTTG 1740  
 QY 2216 AGATGCTGTGAGGAGCAACGAGAAATTTGTGTACTGACATGAGGAAGTGAATTTGCGAG 2275  
 DB 1741 AGATGCTGTGAGGAGCAACGAGAAATTTGTGTACTGACATGAGGAAGTGAATTTGCGAG 1800







QY 1856 ACCTCGAAGAGCATGCTGCTATTCACCTTGAAATAGTTCCTCTATTTTGAACGAGCTGG 1915  
 DB 1381 ACCTCGAAGAGCATGCTGCTATTCACCTTGAAATAGTTCCTCTATTTTGAACGAGCTGG 1440  
 QY 1916 CGGATAGAGAGGCGGTGTTTACTGTGATACCGGACATGTCGAATGTGCAATCGAGGT 1975  
 DB 1441 CGGATAGAGAGGCGGTGTTTACTGTGATACCGGACATGTCGAATGTGCAATCGAGGT 1500  
 QY 1976 ACATCGAAGATCCGAGAGGAAACGCGCACTTTGTGGTTCATTTCCGCAACGCGACGATGG 2035  
 DB 1501 ACATCGAAGATCCGAGAGGAAACGCGCACTTTGTGGTTCATTTCCGCAACGCGACGATGG 1560  
 QY 2036 CTAATGCGTTCCTCATGCGATGCTGCGCAAGTGTGATCGAAGCCGCGAGGTGATCG 2095  
 DB 1561 CTAATGCGTTCCTCATGCGATGCTGCGCAAGTGTGATCGAAGCCGCGAGGTGATCG 1620  
 QY 2096 CGATGTGTGCGCATGCTGCTTTGGGCAATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTGC 2155  
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 QY 2156 ACCAATTCGCGTGAAGGCTGTGCTTTTAAACAAGTTCCTTTGGGCAATGCTGAAGTTGG 2215  
 DB 1681 ACCAATTCGCGTGAAGGCTGTGCTTTTAAACAAGTTCCTTTGGGCAATGCTGAAGTTGG 1740  
 QY 2216 AGATGCTGCTGAGAGGCAAGCAGCAATTTGTGTAACAATGAGAAAGTGAATTTCCAG 2275  
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 QY 2336 AGCAGTAGCTGAGGCGATTTGGCATATCTGTGACCTGTACTGATGATATGCTCAAGATC 2395  
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 QY 2396 CTAATGCGTTCCTCATGCGATGCTGCGCAACATCACTGCTGATGCTGATGCTGATGCTG 2455  
 DB 1921 CTAATGCGTTCCTCATGCGATGCTGCGCAACATCACTGCTGATGCTGATGCTGATGCTG 1980  
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 DB 1981 CGGCGACCCGAAACCGTCTTTGTGAGAGAGTGAAGAGGATGATGATGCTGCGCGTTCGA 2040  
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 DB 2101 GCGCTTAAGTGCACATTTCCAGAGATGAGAGCTCAGCGCGGTGCCATGAGATTGCGCT 2160

; LENGTH: 2160  
 ; TYPE: DNA  
 ; ORGANISM: Corynebacterium glutamicum  
 ; FEATURES:  
 ; NAME/KEY: CDS  
 ; LOCATION: (327)..(2063)  
 ; OTHER INFORMATION: poxb  
 US-10-686-736-4  
 Query Match 66.5%; Score 2160; DB 16; Length 2160;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 476 TTAGAGGCGATTCCTGTGAGGTCACTTTTGTGGGCTGCGGGTCTAAATTTGGCCAGTTT 535  
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 QY 716 AAGCGTGCAACAATCTGAATTTAAGAGCAATTAAGTTCGACCAAGTTAGGCAAC 775  
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 QY 776 AATAGCCATAGCTTGAAGGATTCAGATGCGACACAGCTACGCAAGCAATTAATGACA 835  
 DB 301 AATAGCCATAGCTTGAAGGATTCAGATGCGACACAGCTACGCAAGCAATTAATGACA 360  
 QY 836 CTTTGAAGCTCAAGGTGTGAAGGAAATTAAGTTTGTGGGTGACAGGCTTAATCGA 895  
 DB 361 CTTTGAAGCTCAAGGTGTGAAGGAAATTAAGTTTGTGGGTGACAGGCTTAATCGA 420  
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 DB 421 TCGTGATGCTGTCCGCAATCAGATTAAGTGAAGTGCACGTTTCAATGAAGAGACGG 480  
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 DB 481 CGGCGTTTGCAGCGCGTGGCGAATCGTTGATCACTGCGGAGCTGGCAGTATGTGCTCT 540  
 QY 1016 CTTGTGCTCCTGGAACAACAACACTGATTCAGAGGCTCTTAATGATTCGAAATGATG 1075  
 DB 541 CTTGTGCTCCTGGAACAACAACACTGATTCAGAGGCTCTTAATGATTCGAAATGATG 600  
 QY 1076 CGAAGTGTGGCCATGCTAGCCATATTCAGAGTCCAGATTTGTTCACGTTCTTCC 1135  
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 DB 661 AGAAGAGCATCCGAGATTTTGTAAAGAAATGCTGTGTTACTGCGAAGTGTGAATG 720  
 QY 1196 GTGTGAGAGCGGTGGAACGATTTTGAATCAACGATTCAGTCCACCATGCGGTAAAG 1255  
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 QY 1256 GTGTGTCGTGTGATGATCTCTGTGATATCTCTAAGAAAGACGAGTGAAGCTTCTT 1315  
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 QY 1316 ATTCCAAATTCACATATTTCTTGTGGAATCTGTGTGTTCCGGAATCTACTGAGGCTG 1375  
 DB 841 ATTCCAAATTCACATATTTCTTGTGGAATCTGTGTGTTCCGGAATCTACTGAGGCTG 900

RESULT 8  
 US-10-686-736-4  
 ; Sequence 4, Application US/10686736  
 ; Publication No. US20040063181A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dunigan, Rita  
 ; APPLICANT: McCormack, Ashling  
 ; APPLICANT: Stapleton, Cliona  
 ; APPLICANT: Burke, Kevin  
 ; APPLICANT: Moeckel, Bettina  
 ; TITLE OF INVENTION: Process for the preparation of L-amino acids using  
 ; TITLE OF INVENTION: a gene encoding 6-phosphogluconate Dehydrogenase  
 ; FILE REFERENCE: 990229 BT-US-B  
 ; CURRENT APPLICATION NUMBER: US/10/686,736  
 ; CURRENT FILING DATE: 2003-10-17  
 ; PRIOR APPLICATION NUMBER: US/10/078,167A  
 ; PRIOR FILING DATE: 2002-02-22  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 4

QY 1376 CAGCGCTGTGAGGCGCATTAACAAGCCTAAGTCTGCTCACTTTGTTCTGCGGTGCGGCG 1435  
 DB 901 CAGGCGCTGTGAGGCGCATTAACAAGCCTAAGTCTGCTCACTTTGTTCTGCGGTGCGGCG 960  
 QY 1436 TGAAGATGCTCCGCGCGGAGGTGTTGAGTGGCGGAGAAATTAATCAACCATCCGGC 1495  
 DB 961 TGAAGATGCTCCGCGCGGAGGTGTTGAGTGGCGGAGAAATTAATCAACCATCCGGC 1020  
 QY 1496 ATGCGCTGGGTGAGTGAACAGTACATCCAGCATGAGAAATCCGTTGAGGTGCGCATGCTG 1555  
 DB 1021 ATGCGCTGGGTGAGTGAACAGTACATCCAGCATGAGAAATCCGTTGAGGTGCGCATGCTG 1080  
 QY 1556 GCCTGCTGTTGATCGCGCGCTGCTGATGCTCAATGAGGCGGATCTGCTGATTTAT 1615  
 DB 1081 GCCTGCTGTTGATCGCGCGCTGCTGATGCTCAATGAGGCGGATCTGCTGATTTAT 1140  
 QY 1616 TGGGTACGAAATTCCTTATTTGATTTCTTCTTAAGAACAAGTTGCCAGGTGATA 1675  
 DB 1141 TGGGTACGAAATTCCTTATTTGATTTCTTCTTAAGAACAAGTTGCCAGGTGATA 1200  
 QY 1676 TCAACGCTGCGCATATGCTGCAAGTACACGCGTGAAGTATCCGCTGACCGGTGATGTTG 1735  
 DB 1201 TCAACGCTGCGCATATGCTGCAAGTACACGCGTGAAGTATCCGCTGACCGGTGATGTTG 1260  
 QY 1736 CTGCAACATCGAAATATTTTGTCTCATGTGAAGAAAAACAGATGCTTCTCTTG 1795  
 DB 1261 CTGCAACATCGAAATATTTTGTCTCATGTGAAGAAAAACAGATGCTTCTCTTG 1320  
 QY 1796 ATGGATGCTCAAGGCGCAGAGGCTAAGTGAAGTCTGGGTGATGAGAACTTAACACATA 1855  
 DB 1321 ATGGATGCTCAAGGCGCAGAGGCTAAGTGAAGTCTGGGTGATGAGAACTTAACACATA 1380  
 QY 1856 ACCTGCAAGAGCATGTGCTTATTCACCTGAAATACGTTGCTCATTTTGAACGAGCTG 1915  
 DB 1381 ACCTGCAAGAGCATGTGCTTATTCACCTGAAATACGTTGCTCATTTTGAACGAGCTG 1440  
 QY 1916 CGGATTAAGATGCGGTGTTTACTGTGATACCGGATGTGCAATGTGTGCAATGCAAGT 1975  
 DB 1441 CGGATTAAGATGCGGTGTTTACTGTGATACCGGATGTGCAATGTGTGCAATGCAAGT 1500  
 QY 1976 ACATCGAATCGGAGGAGGAGGAGCGGAGCTTTGGGTGATTAATCCGCAAGGACGATG 2035  
 DB 1501 ACATCGAATCGGAGGAGGAGGAGCGGAGCTTTGGGTGATTAATCCGCAAGGACGATG 1560  
 QY 2036 CTATGCGTGTCTCATGCGATGTGTGCGCAAGTGTGATCGAAACCGCAGGTGATG 2095  
 DB 1561 CTATGCGTGTCTCATGCGATGTGTGCGCAAGTGTGATCGAAACCGCAGGTGATG 1620  
 QY 2096 CGATGTGTGCGCATGTGTGTTGGGCGATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTG 2155  
 DB 1621 CGATGTGTGCGCATGTGTGTTGGGCGATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTG 1680  
 QY 2156 ACCAATCTTCGCGTGAAGGCGTGTGTGTTAAACAAGTCTTTGGGCGATGTGAAGTGG 2215  
 DB 1681 ACCAATCTTCGCGTGAAGGCGTGTGTGTTAAACAAGTCTTTGGGCGATGTGAAGTGG 1740  
 QY 2216 AGATGCTGTGAGGAGGAGCAACGAAATTTGTACTGACATGAGGAAGTGAATTTGCA 2275  
 DB 1741 AGATGCTGTGAGGAGGAGCAACGAAATTTGTACTGACATGAGGAAGTGAATTTGCA 1800  
 QY 2276 AGATGCGCGGCGTGGGCTGATCAATCGGTACGATCACCGATCCGAGAAAGTTGCG 2335  
 DB 1801 AGATGCGCGGCGTGGGCTGATCAATCGGTACGATCACCGATCCGAGAAAGTTGCG 1860  
 QY 2336 AGCAGCTAGCTGAGGAGTGGCATATCTGAGCTGATCGATCGATATCTGATCGGATC 2395  
 DB 1861 AGCAGCTAGCTGAGGAGTGGCATATCTGAGCTGATCGATCGATATCTGATCGGATC 1920  
 QY 2396 CTATATGCGCTGTGATCCCAACCAACATCATCGTGGGAACAGTCAATGGATTCAGCAAG 2455  
 DB 1921 CTATATGCGCTGTGATCCCAACCAACATCATCGTGGGAACAGTCAATGGATTCAGCAAG 1980  
 QY 2456 CGGCGACCGGACCGTCTTTGTTGAGAGAGTGAAGAGCATGATCATCTGCGCCGTTCA 2515

DB 1981 CGGCGACCGGACCGTCTTTGTGAGAGTGAAGAGGATGATCGATCTGCGGTTGCA 2040  
 QY 2516 ACATTAAGAAATATTTCTTCACTCCATGATGATTAATTAACCTGCTGTTCTCATTAACCGCA 2575  
 DB 2041 ACATTAAGAAATATTTCTTCACTCCATGATGATTAATTAACCTGCTGTTCTCATTAACCGCA 2100  
 QY 2576 GCGCTTAAGTGAACATTTCCAGATGAGGAGCTCAAGCGCGGTGCCATGAGATGGCT 2635  
 DB 2101 GCGCTTAAGTGAACATTTCCAGATGAGGAGCTCAAGCGCGGTGCCATGAGATGGCT 2160

RESULT 9  
 US-10-781-014-85  
 ; Sequence 85, Application US/10781014  
 ; Publication No. US20040180408A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pompejus, Markus  
 ; APPLICANT: Kroger, Burhard  
 ; APPLICANT: Schroder, Hartwig  
 ; APPLICANT: Zelder, Oskar  
 ; APPLICANT: Haberer, Gregor  
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
 ; TITLE OF INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY  
 ; FILE REFERENCE: BGI-126CPN  
 ; CURRENT APPLICATION NUMBER: US/10/781,014  
 ; CURRENT FILING DATE: 2004-02-17  
 ; PRIOR APPLICATION NUMBER: US 09/602,740  
 ; PRIOR FILING DATE: 2000-06-23  
 ; PRIOR APPLICATION NUMBER: 60/141,031  
 ; PRIOR FILING DATE: 1999-06-25  
 ; PRIOR APPLICATION NUMBER: 60/143,208  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: 60/151,572  
 ; PRIOR FILING DATE: 1999-08-31  
 ; PRIOR APPLICATION NUMBER: DE 19931412.8  
 ; PRIOR FILING DATE: 1999-07-08  
 ; PRIOR APPLICATION NUMBER: DE 19931413.6  
 ; PRIOR FILING DATE: 1999-07-08  
 ; PRIOR APPLICATION NUMBER: DE 19931419.5  
 ; PRIOR FILING DATE: 1999-07-08  
 ; PRIOR APPLICATION NUMBER: DE 19931420.9  
 ; PRIOR FILING DATE: 1999-07-08  
 ; PRIOR APPLICATION NUMBER: DE 19931424.1  
 ; PRIOR FILING DATE: 1999-07-08  
 ; PRIOR APPLICATION NUMBER: DE 19931428.4  
 ; PRIOR FILING DATE: 1999-07-08  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 784  
 ; SEQ ID NO 85  
 ; LENGTH: 1860  
 ; TYPE: DNA  
 ; ORGANISM: Corynebacterium glutamicum  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (101)..(1837)  
 ; OTHER INFORMATION: RXN00635  
 US-10-781-014-85

Query Match 57.3%; Score 1860; DB 17; Length 1860;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1860; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 702 CTGGCAGGGGCGGAGGCTGGCAACAATGGAATTTAAGACACAATTAAGTGGCAC 761  
 DB 1 CTGGCAGGGGCGGAGGCTGGCAACAATGGAATTTAAGACACAATTAAGTGGCAC 60  
 QY 762 AAGTAGCAACACATATACCATTAAGTGAAGAGTTCAGATGGCAACAGCTACGAC 821  
 DB 61 AAGTAGCAACACATATACCATTAAGTGAAGAGTTCAGATGGCAACAGCTACGAC 120  
 QY 822 ACATTAATTAACAATTTGGAAGTCAAGGTGGAAGCAATTTATGTTGGTGGTGA 881

Db 121 ACAATTAAATTGACACTTTGAAAGCTCAAGGTGTGAACGAATTTATGTTGGTGTGA 180  
 Qy 882 CAGCTTAATCCGATGTGATGCTGTCCGCAATCAGATTAAGTGGGTCAGTTGG 941  
 Db 181 CAGCTTAATCCGATGTGATGCTGTCCGCAATCAGATTAAGTGGGTCAGTTGG 240  
 Qy 942 AAATGAGAAAGCGCGCTTTTGGACCGGTGCGAAATGCTTGAATCACTGGAGTGGC 1001  
 Db 241 AAATGAGAAAGCGCGCTTTTGGACCGGTGCGAAATGCTTGAATCACTGGAGTGGC 300  
 Qy 1002 AGATATGCTGCTTCTTGTGTCTGTGAAAACAACACTGATTCAGGGTCTTTATGATTC 1061  
 Db 301 AGATATGCTGCTTCTTGTGTCTGTGAAAACAACACTGATTCAGGGTCTTTATGATTC 360  
 Qy 1062 GCATCGAAATGAGTGGCAAGGTGTGGCATCGCTGACGATTCCTGAGTCCCGAATTTGG 1121  
 Db 361 GCATCGAAATGAGTGGCAAGGTGTGGCATCGCTGACGATTCCTGAGTCCCGAATTTGG 420  
 Qy 1122 TTGACGTTCTTCCAGGAAACGATCCGAGATTTTGAAGAAATGCTGTGGTTACTG 1181  
 Db 421 TTGACGTTCTTCCAGGAAACGATCCGAGATTTTGAAGAAATGCTGTGGTTACTG 480  
 Qy 1182 CGAGATGTGAATGTGTGTGAGCAAGGTGAACGCAATTTGCAATCAGCGATTCAGTCCAC 1241  
 Db 481 CGAGATGTGAATGTGTGTGAGCAAGGTGAACGCAATTTGCAATCAGCGATTCAGTCCAC 540  
 Qy 1242 CAGGCGGGGTAAAGGTGTGTGCGGTGAGTGAATTCCTGAGTGAATTCGCTTAAGAAAGCGC 1301  
 Db 541 CAGGCGGGGTAAAGGTGTGTGCGGTGAGTGAATTCCTGAGTGAATTCGCTTAAGAAAGCGC 600  
 Qy 1302 AGGTGAACGTAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 1361  
 Db 601 AGGTGAACGTAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 660  
 Qy 1362 TCTTACTGAGGCTGCAAGCGCTGTGTGAAGGCGATTAACACGCTAAGTCTGTCACTTTGTT 1421  
 Db 661 TCTTACTGAGGCTGCAAGCGCTGTGTGAAGGCGATTAACACGCTAAGTCTGTCACTTTGTT 720  
 Qy 1422 CTCGCGGTGCGGGGTGAAGAAATGCTGCGCGCGAGTGTGAGATTTGGCGGAAAGATTA 1481  
 Db 721 CTCGCGGTGCGGGGTGAAGAAATGCTGCGCGCGAGTGTGAGATTTGGCGGAAAGATTA 780  
 Qy 1482 ATCACCAGATCGGGCATGCGCTGGGTGTGAAGAGTACATCAGCATGAGAAATCCGTTGA 1541  
 Db 781 ATCACCAGATCGGGCATGCGCTGGGTGTGAAGAGTACATCAGCATGAGAAATCCGTTGA 840  
 Qy 1542 GGTGCGCATGTGCGCTGTGTGAAGGCGCTGTGTGAAGTGTGCAATGAGCGGA 1601  
 Db 841 GGTGCGCATGTGCGCTGTGTGAAGGCGCTGTGTGAAGTGTGCAATGAGCGGA 900  
 Qy 1602 TCTGCTGATTCATTTGGGTACGGAATTCCTTATTCGATTTCTTCTTAAAGCAAGT 1661  
 Db 901 TCTGCTGATTCATTTGGGTACGGAATTCCTTATTCGATTTCTTCTTAAAGCAAGT 960  
 Qy 1662 TGGCCAGGTGAGTATCAAGGTGCGCATTTGTCAGCGTACACAGGTGAAGTATCCGGT 1721  
 Db 961 TGGCCAGGTGAGTATCAAGGTGCGCATTTGTCAGCGTACACAGGTGAAGTATCCGGT 1020  
 Qy 1722 GACCGGTGATGTGTGTCACAAATTCGAAATATTTTTCCTCATGTGAAGAAACAG 1781  
 Db 1021 GACCGGTGATGTGTGTCACAAATTCGAAATATTTTTCCTCATGTGAAGAAACAG 1080  
 Qy 1782 TCGTTCTTCTTGTGATGTGATGCTCAAGGCAACAGAGCTGAAGTGAAGTGTGTGA 1841  
 Db 1081 TCGTTCTTCTTGTGATGTGATGCTCAAGGCAACAGAGCTGAAGTGAAGTGTGTGA 1140  
 Qy 1842 GAGTACACATTAAGTGAAGAAAGTGTGCTATTCCTGAATGAGTGTGTGTAT 1901  
 Db 1141 GAGTACACATTAAGTGAAGAAAGTGTGCTATTCCTGAATGAGTGTGTGTAT 1200  
 Qy 1902 TTGAAAGAGCTGCGGATTAAGATGCGTGTACTGTGATTAACCGCATGTGCATGT 1961

Db 1201 TTGAAAGAGCTGCGGATTAAGATGCGGTGTACTGTGTGAATCCGCGCATGTGCATGT 1260  
 Qy 1962 GTGCGATGAGAGTATCATTCAGAAATCCGAGAGGAACGCGCACTTTGTGGTCAATTCG 2021  
 Db 1261 GTGCGATGAGAGTATCATTCAGAAATCCGAGAGGAACGCGCACTTTGTGGTCAATTCG 1320  
 Qy 2022 CCAAGGACGATGTATATGCTGTGCTCATGCGATTTGTGCGAAAGTGTGATCGAA 2081  
 Db 1321 CCAAGGACGATGTATATGCTGTGCTCATGCGATTTGTGCGAAAGTGTGATCGAA 1380  
 Qy 2082 CCGCGAGATGATGCGATGTGTGCGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2141  
 Db 1381 CCGCGAGATGATGCGATGTGTGCGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440  
 Qy 2142 GACCGTAACTGACCAACTCCGCTGAGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2201  
 Db 1441 GACCGTAACTGACCAACTCCGCTGAGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500  
 Qy 2202 CATGTGAGATGTGAATGCTGTGTGAGGACAGCCAGAAATTTGTGATCTGACATGAGA 2261  
 Db 1501 CATGTGAGATGTGAATGCTGTGTGAGGACAGCCAGAAATTTGTGATCTGACATGAGA 1560  
 Qy 2262 AGTGAATTTGCGAGATGTGCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2321  
 Db 1561 AGTGAATTTGCGAGATGTGCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620  
 Qy 2322 GAAGAAAGTTGCGAGAGCTAGCTGAGGATTTGCGATTCCTGAGACTGTGATCTGATCGA 2381  
 Db 1621 GAAGAAAGTTGCGAGAGCTAGCTGAGGATTTGCGATTCCTGAGACTGTGATCTGATCGA 1680  
 Qy 2382 TATGTCACGATCTTATATGCGCTGTGTGATCCACCAACCATCATCGTGGAAACAGTCA 2441  
 Db 1681 TATGTCACGATCTTATATGCGCTGTGTGATCCACCAACCATCATCGTGGAAACAGTCA 1740  
 Qy 2442 GGAATTCAGCAAGCGGCGCACCCGAAACGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGT 2501  
 Db 1741 GGAATTCAGCAAGCGGCGCACCCGAAACGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1800  
 Qy 2502 TCTGCGCCGTTCCAAATTAAGAAATATTCCTACTCCATGATGATTAACCTGCTGTT 2561  
 Db 1801 TCTGCGCCGTTCCAAATTAAGAAATATTCCTACTCCATGATGATTAACCTGCTGTT 1860

RESULT 10  
 US-09-738-626-2873  
 ; Sequence 2873, Application US/09738626  
 ; Publication No. US20020197605A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NAKAGAWA, SATOSHI  
 ; APPLICANT: MIZOGUCHI, HIROSHI  
 ; APPLICANT: ANDO, SEIKO  
 ; APPLICANT: HAYASHI, MIKIRO  
 ; APPLICANT: OCHIALI, KEIRO  
 ; APPLICANT: YOKOI, HARUHIKO  
 ; APPLICANT: TATEISHI, NAOKO  
 ; APPLICANT: SENOH, AKIHIRO  
 ; APPLICANT: IKEDA, MASATO  
 ; APPLICANT: OZAKI, AKIO  
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 ; FILE REFERENCE: 249-125  
 ; CURRENT APPLICATION NUMBER: US/09/738, 626  
 ; CURRENT FILING DATE: 2000-12-18  
 ; PRIOR APPLICATION NUMBER: JP 99/377484  
 ; PRIOR FILING DATE: 1999-12-16  
 ; PRIOR APPLICATION NUMBER: JP 00/159162  
 ; PRIOR FILING DATE: 2000-04-07  
 ; PRIOR APPLICATION NUMBER: JP 00/280988  
 ; PRIOR FILING DATE: 2000-08-03  
 ; NUMBER OF SEQ ID NOS: 7059  
 ; SOFTWARE: PatentIn ver. 3.0  
 ; SEQ ID NO 2873  
 ; LENGTH: 1737  
 ; TYPE: DNA

ORGANISM: *Corynebacterium glutamicum*  
US-09-738-626-2873

Query Match 53.5%; Score 1737; DB 9; Length 1737;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 1737; Conservative 0; Indels 0; Gaps 0;

QY 802 ATGGCACAAGCTACGAGAACATTAATTGCACTTTGGAAGCTCAAGGTGTAACGA 861  
DB 1 ATGGCACAAGCTACGAGAACATTAATTGCACTTTGGAAGCTCAAGGTGTAACGA 60  
QY 862 ATTATATGTTGGTGGGTGACAGCCTTAATCCATCGTGAATGCTGTCCGCAATCAAT 921  
DB 61 ATTATATGTTGGTGGGTGACAGCCTTAATCCATCGTGAATGCTGTCCGCAATCAAT 120  
QY 922 ATTGAGTGGGTGACGTTTCGAAATGAGAAAGCGCGGGCTTTGAGCGCGGTGCGGAATCG 981  
DB 121 ATTGAGTGGGTGACGTTTCGAAATGAGAAAGCGCGGGCTTTGAGCGCGGTGCGGAATCG 180  
QY 982 TTGATCACTGGGAGCTGGGAGATGTCGTCTTCTTGAGTCTGGAACAACAACCTG 1041  
DB 181 TTGATCACTGGGAGCTGGGAGATGTCGTCTTCTTGAGTCTGGAACAACAACCTG 240  
QY 1042 ATTCAAGGCTCTTATGATGTCGATCGAAATGCTGCGAAGGTGTTGSCATGCTAGCCAT 1101  
DB 241 ATTCAAGGCTCTTATGATGTCGATCGAAATGCTGCGAAGGTGTTGSCATGCTAGCCAT 300  
QY 1102 ATTCGAGTGGCCGAGATTGGTTCGACGTTCTTCCAGGAAACGATCCGAGATTTGTTT 1161  
DB 301 ATTCGAGTGGCCGAGATTGGTTCGACGTTCTTCCAGGAAACGATCCGAGATTTGTTT 360  
QY 1162 AAGGAATGCTCTGGTACTGCGAGATGATGATGATGATGATGATGATGATGATGATGAT 1221  
DB 361 AAGGAATGCTCTGGTACTGCGAGATGATGATGATGATGATGATGATGATGATGATGAT 420  
QY 1222 CATCAAGCCTTCAATGTCACATGCGCGGTAAAGGTGTGTCGGTGGTATGATTTCTGGT 1281  
DB 421 CATCAAGCCTTCAATGTCACATGCGCGGTAAAGGTGTGTCGGTGGTATGATTTCTGGT 480  
QY 1282 GATATGCTTAAAGAAAGACGAGGTGACGCTACTTAATTCATTCATTAATTTCTCGGC 1341  
DB 481 GATATGCTTAAAGAAAGACGAGGTGACGCTACTTAATTCATTCATTAATTTCTCGGC 540  
QY 1342 ACTCTGTGTGTGTTCCCGATCTTACTGAGGCTGACGCGTGTGTGAGGCGGATTAACAAC 1401  
DB 541 ACTCTGTGTGTGTTCCCGATCTTACTGAGGCTGACGCGTGTGTGAGGCGGATTAACAAC 600  
QY 1402 GCTAAGTCTGCTCTTTGTTCTGCGGTGCGGGGTGAAGAAATCTGCGCGCAGGTGTTG 1461  
DB 601 GCTAAGTCTGCTCTTTGTTCTGCGGTGCGGGGTGAAGAAATCTGCGCGCAGGTGTTG 660  
QY 1462 GAGTTGGCGGAGAAATTAATCAACGATCGGCGCATGCGTGGGTGTAGAGCATATC 1521  
DB 661 GAGTTGGCGGAGAAATTAATCAACGATCGGCGCATGCGTGGGTGTAGAGCATATC 720  
QY 1522 CAGCATGAGAAATCGTTTGAAGTCGCGATGTCGTGCTGTGTTACGCGCTGCGTG 1581  
DB 721 CAGCATGAGAAATCGTTTGAAGTCGCGATGTCGTGCTGTGTTACGCGCTGCGTG 780  
QY 1582 GATGCGTCCAAATGAGCGGATCTGCTGATTTCTATTGGGTACGGAATTTCCCTATTCTGAT 1641  
DB 781 GATGCGTCCAAATGAGCGGATCTGCTGATTTCTATTGGGTACGGAATTTCCCTATTCTGAT 840  
QY 1642 TTCTCTCTTAAAGAACAGCTTGGCCAGGTGATATCAACGCGTGGCATGTTGTCAGCT 1701  
DB 841 TTCTCTCTTAAAGAACAGCTTGGCCAGGTGATATCAACGCGTGGCATGTTGTCAGCT 900  
QY 1702 ACCACGGTGAAGTATCCGCTGACCGGTGATGTTGCTGCAACAATCGAAATATTTTGCT 1761  
DB 901 ACCACGGTGAAGTATCCGCTGACCGGTGATGTTGCTGCAACAATCGAAATATTTTGCT 960  
QY 1762 CATGTAAGAGAAAAACAATGTTCTTCTTATCGATGCTCAAGGACACAGAGCT 1821

DB 961 CATGTAAGAGAAAAACAATGCTTCTTCTTATCGATGCTCAAGGACACAGAGCT 1020  
QY 1822 AAGTTGAGCTCGGTGTGTAAGAGATGACACATTAAGTGAAGAAAGATGCTTATTCAC 1881  
DB 1021 AAGTTGAGCTCGGTGTGTAAGAGATGACACATTAAGTGAAGAAAGATGCTTATTCAC 1080  
QY 1882 CCTGAATACGTTCCCTCTATTATTTGAACGAGCTGGCGGATTAAGATCGGGTGTACTGTG 1941  
DB 1081 CCTGAATACGTTCCCTCTATTATTTGAACGAGCTGGCGGATTAAGATCGGGTGTACTGTG 1140  
QY 1942 GATACCGGATGTCATGATGTGTGCAATGCGAGGTACATGAGAAATCCGAGGAAACGCGC 2001  
DB 1141 GATACCGGATGTCATGATGTGTGCAATGCGAGGTACATGAGAAATCCGAGGAAACGCGC 1200  
QY 2002 GACTTGTGGGTTCATTCGCGCAACGCGGATGCGCTTAATGCGTGTGCTATGAGATTTGCT 2061  
DB 1201 GACTTGTGGGTTCATTCGCGCAACGCGGATGCGCTTAATGCGTGTGCTATGAGATTTGCT 1260  
QY 2062 GCGCAAGTGTGATGCAAAACGCGAGTGTATCGCATGTGTGCGATGCTGTTGGGC 2121  
DB 1261 GCGCAAGTGTGATGCAAAACGCGAGTGTATCGCATGTGTGCGATGCTGTTGGGC 1320  
QY 2122 ATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTGACCAACTTCCGCTGAAGGCTGTGTG 2181  
DB 1321 ATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTGACCAACTTCCGCTGAAGGCTGTGTG 1380  
QY 2182 TTTAACAAGTCTTTTGGGCAATGTAAGTGTGAGATGCTGTGTGAGGAGACAGCCAGA 2241  
DB 1381 TTTAACAAGTCTTTTGGGCAATGTAAGTGTGAGATGCTGTGTGAGGAGACAGCCAGA 1440  
QY 2242 TTTGTAAGTACCAATGAGAAATTTTCCAGAGATTTGCGGCGCTCGGCTATCAAA 2301  
DB 1441 TTTGTAAGTACCAATGAGAAATTTTCCAGAGATTTGCGGCGCTCGGCTATCAAA 1500  
QY 2302 TGGTACGATCAACGATCCGAAAGATTTGCGAGCACTGATGAGGATTTGGCATAT 2361  
DB 1501 TGGTACGATCAACGATCCGAAAGATTTGCGAGCACTGATGAGGATTTGGCATAT 1560  
QY 2362 CCTGACCTGTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2421  
DB 1561 CCTGACCTGTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620  
QY 2422 ATCAGTGGGAAACAGTCAATGGAATTCAGCAAGCGGCAACCGACGCTTTTGTGGA 2481  
DB 1621 ATCAGTGGGAAACAGTCAATGGAATTCAGCAAGCGGCAACCGACGCTTTTGTGGA 1680  
QY 2482 GAGTGAAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2538  
DB 1681 GAGTGAAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1737

RESULT 11  
US-10-781-014-89  
Sequence 89, Application US/10781014  
Publication No. US20040180408A1  
GENERAL INFORMATION:  
APPLICANT: Pompeius, Markus  
APPLICANT: Schroder, Burkhard  
APPLICANT: Zelder, Oskar  
APPLICANT: Haberhauser, Gregor  
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
TITLE OF INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY  
FILE REFERENCE: BGI-126PCN  
CURRENT APPLICATION NUMBER: US/10/781,014  
CURRENT FILING DATE: 2004-02-17  
PRIOR APPLICATION NUMBER: US 09/602,740  
PRIOR FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: 60/141,031  
PRIOR FILING DATE: 1999-06-25  
PRIOR APPLICATION NUMBER: 60/143,208  
PRIOR FILING DATE: 1999-07-09











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Db      661 GAGACGTACACACATTAACGTGAGAACATGTCCTATTCACCCTGAATACGTTGCCTT 720
Qy      1900 ATTTGAAACGAGCTGGCGGATTAAGATGCGGTGTTACTGTGATACCGGCATGTGCAAT 1959
Db      721 ATTTGAAACGAGCTGGCGGATTAAGATGCGGTGTTACTGTGATACCGGCATGTGCAAT 780
Qy      1960 GTGTGCATGCGAGGTACATCGAGAAATCCGAGAGGAAACGCGCATTTGTGGGTTCAATC 2019
Db      781 GTGTGCATGCGAGGTACATCGAGAAATCCGAGAGGAAACGCGCATTTGTGGGTTCAATC 840
Qy      2020 CGCCACGGCACGATGGCTAAATGCTTGCTCATGC 2054
Db      841 CGCCACGGCACGATGGCTAAATGCTTGCTCATGC 875
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Search completed: January 15, 2005, 14:58:42  
Job time : 1682.44 secs